

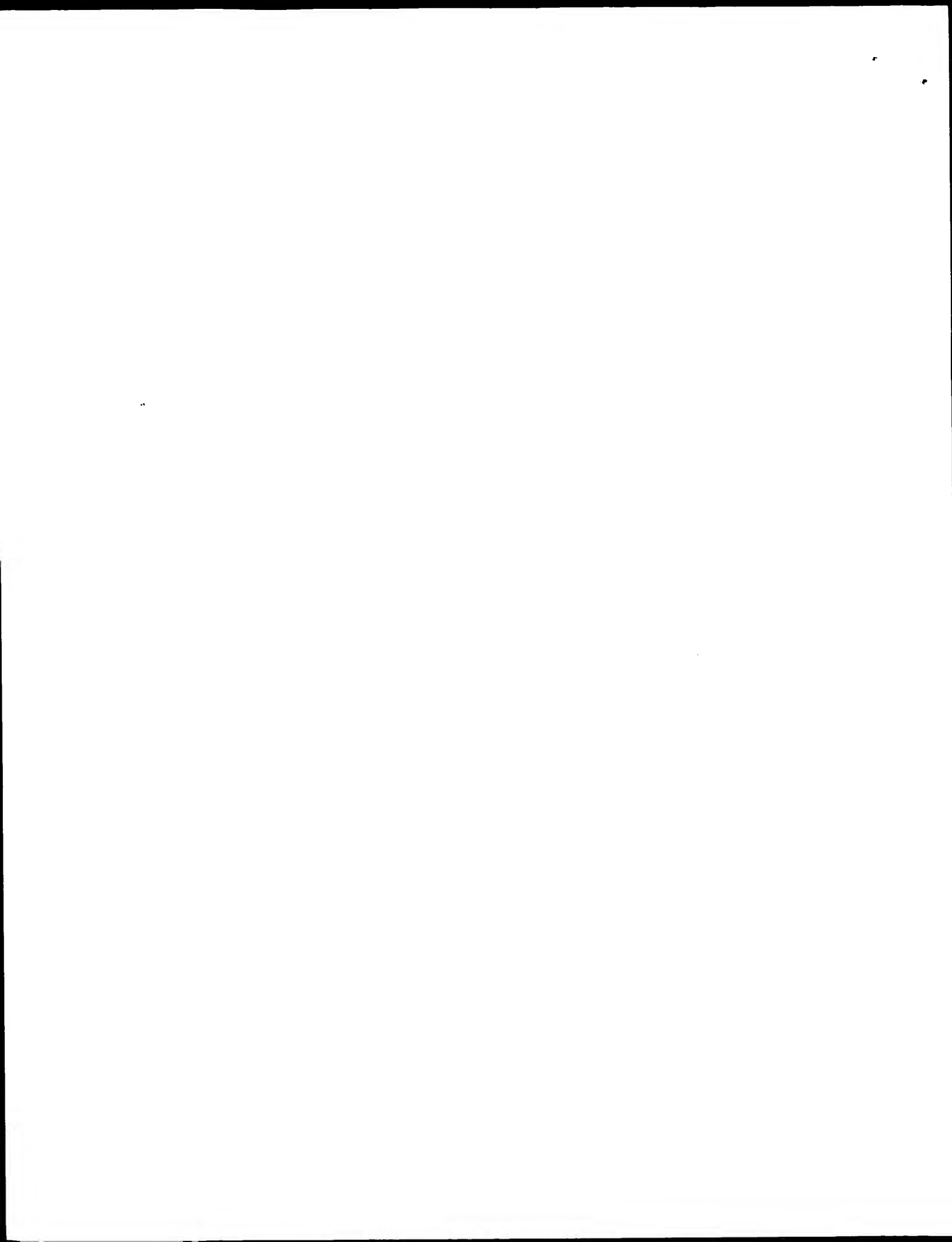
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(54) Title: METHOD TO DETECT CANINE IgE (57) Abstract <p>The present invention includes a method to detect canine IgE using a canine Fc epsilon receptor (FcεR) to detect canine IgE antibodies in a biological sample from a canid. The present invention also relates to kits to perform such methods.</p>		



## METHOD TO DETECT CANINE IgE

## Field of the Invention

The present invention relates to a novel method to detect canine epsilon immunoglobulin (IgE). The present invention also includes novel kits to detect canine  
5 IgE as well as methods to produce the detection reagent.

## Background of the Invention

Diagnosis of disease and determination of treatment efficacy are important tools in medicine. In particular, detection of IgE production in an animal can be indicative of disease. Such diseases include, for example, allergy, atopic disease, hyper IgE  
10 syndrome, internal parasite infections and B cell neoplasia. In addition, detection of IgE production in an animal following a treatment is indicative of the efficacy of the treatment, such as when using treatments intended to disrupt IgE production.

Until the discovery of the present invention, detection of IgE in samples obtained from non-human animals has been hindered by the absence of suitable reagents for  
15 detection of IgE. Various compounds have been used to detect IgE in IgE-containing compositions. In particular, antibodies that bind selectively to epsilon idiotype antibodies (i.e., anti-IgE antibodies) have been used to detect IgE. These anti-IgE antibodies, however, can cross-react with other antibody idiotypes, such as gamma isotype antibodies. The discovery of the present invention includes the use of a canine  
20 Fc epsilon receptor (Fc<sub>ε</sub>R) molecule to detect the presence of IgE in a putative IgE-containing composition. Canine high affinity Fc<sub>ε</sub>R consists of three protein chains, alpha, beta and gamma. Hayashi et al. have disclosed the nucleic acid sequence for the alpha chain (GenBank Accession No. D16413, submitted June 8, 1993). A canine Fc<sub>ε</sub>R molecule provides an advantage over, for example anti-IgE antibodies, to detect IgE  
25 because a canine Fc<sub>ε</sub>R molecule can bind to a canine IgE with more specificity (i.e., less idiotype cross-reactivity) and more sensitivity (i.e., affinity) than anti-IgE binding antibodies.

Thus, methods and kits are needed in the art that will provide specific detection of canine IgE using canine Fc<sub>ε</sub>R.

### Summary of the Invention

The present invention includes detection methods and kits that detect canine IgE.

One embodiment of the present invention is a method to detect canine IgE comprising: (a) contacting an isolated canine  $Fc_\epsilon$  receptor ( $Fc_\epsilon R$ ) molecule with a putative canine IgE-containing composition under conditions suitable for formation of a  $Fc_\epsilon R$  molecule:IgE complex; and (b) determining the presence of IgE by detecting the  $Fc_\epsilon R$  molecule:IgE complex, the presence of the  $Fc_\epsilon R$  molecule:IgE complex indicating the presence of IgE. In particular, the canine  $Fc_\epsilon R$  molecule comprises at least a portion of a  $Fc_\epsilon R$  alpha chain that binds to canine IgE.

Another embodiment of the present invention is a method to detect canine flea allergy dermatitis comprising: (a) immobilizing a flea allergen on a substrate; (b) contacting the flea allergen with a putative canine IgE-containing composition under conditions suitable for formation of an antigen:IgE complex bound to the substrate; (c) removing non-bound material from the substrate under conditions that retain antigen:IgE complex binding to the substrate; and (d) detecting the presence of the antigen:IgE complex by contacting antigen:IgE complex with a canine  $Fc_\epsilon R$  molecule. In particular, the flea allergen is a flea saliva antigen.

The present invention also includes a kit for performing methods of the present invention. One embodiment is a kit for detecting IgE comprising a canine  $Fc_\epsilon$  receptor ( $Fc_\epsilon R$ ) molecule and a means for detecting canine IgE. Another embodiment is a kit for detecting flea allergy dermatitis comprising a canine  $Fc_\epsilon$  receptor ( $Fc_\epsilon R$ ) molecule and a flea allergen.

### Detailed Description of the Invention

The present invention relates to the discovery that purified high affinity canine Fc epsilon receptor (i.e.,  $Fc_\epsilon RI$ ; referred to herein as  $Fc_\epsilon R$ ) can be used in canine epsilon immunoglobulin (referred to herein as IgE or IgE antibody)-based detection (e.g., diagnostic, screening) methods and kits. The use of canine  $Fc_\epsilon R$  in diagnostic methods and kits is unexpected because the use of canine  $Fc_\epsilon R$  avoids complications presented by use of antibodies that bind to IgE (i.e., anti-IgE antibodies). Such complications include, for example, non-specific binding of anti-IgE antibodies to other classes of immunoglobulin such as gamma immunoglobulin (i.e., IgG).

One embodiment of the present invention is a method to detect a canine IgE using an isolated canine Fc<sub>ε</sub>R molecule. It is to be noted that the term "a" entity or "an" entity refers to one or more of that entity; for example, a protein refers to one or more proteins or at least one protein. As such, the terms "a" (or "an"), "one or more" and "at least one" can be used interchangeably herein. It is also to be noted that the terms "comprising", "including", and "having" can be used interchangeably. Furthermore, a compound "selected from the group consisting of" refers to one or more of the compounds in the list that follows, including mixtures (i.e., combinations) of two or more of the compounds.

10 According to the present invention, an isolated, or biologically pure, Fc<sub>ε</sub>R molecule, is a molecule that has been removed from its natural milieu. As such, "isolated" and "biologically pure" do not necessarily reflect the extent to which the molecule has been purified. An isolated canine Fc<sub>ε</sub>R molecule of the present invention can be obtained from its natural source (e.g., from a canine mast cell), can be produced  
15 using recombinant DNA technology or can be produced by chemical synthesis.

A Fc<sub>ε</sub>R molecule (also referred to herein as Fc<sub>ε</sub>R or Fc<sub>ε</sub>R protein) of the present invention can be a full-length protein, a portion of a full-length protein or any homolog of such a protein, wherein the Fc<sub>ε</sub>R molecule is capable of binding specifically to IgE. As used herein, a protein can be a polypeptide or a peptide. A Fc<sub>ε</sub>R molecule of the  
20 present invention can comprise a complete Fc<sub>ε</sub>R (i.e., alpha, beta and gamma Fc<sub>ε</sub>R chains), an alpha Fc<sub>ε</sub>R chain (also referred to herein as Fc<sub>ε</sub>R α chain) or portions thereof. Preferably, a Fc<sub>ε</sub>R molecule comprises at least a portion of a Fc<sub>ε</sub>R α chain that binds to IgE, i.e., that is capable of forming an immunocomplex with an IgE constant region.

An isolated canine Fc<sub>ε</sub>R molecule of the present invention, including a homolog,  
25 can be identified in a straight-forward manner by the Fc<sub>ε</sub>R molecule's ability to form an immunocomplex with a canine IgE. Examples of Fc<sub>ε</sub>R homologs include Fc<sub>ε</sub>R proteins in which amino acids have been deleted (e.g., a truncated version of the protein, such as a peptide), inserted, inverted, substituted and/or derivatized (e.g., by glycosylation, phosphorylation, acetylation, myristoylation, prenylation, palmitoylation, amidation  
30 and/or addition of glycerophosphatidyl inositol) such that the homolog includes at least one epitope capable of forming an immunocomplex with an IgE.

Fc<sub>ε</sub>R homologs can be the result of natural allelic variation or natural mutation. Fc<sub>ε</sub>R homologs of the present invention can also be produced using techniques known in the art including, but not limited to, direct modifications to the protein or modifications to the gene encoding the protein using, for example, classic or recombinant DNA techniques to effect random or targeted mutagenesis.

According to the present invention, a preferred canine Fc<sub>ε</sub>R α chain of the present invention is encoded by at least a portion of the nucleic acid sequence of the coding strand of a cDNA encoding a full-length Fc<sub>ε</sub>R α chain protein represented herein as SEQ ID NO:19, the portion at least encoding the IgE binding site of the Fc<sub>ε</sub>R α chain protein. Other suitable canine Fc<sub>ε</sub>R α chains useful in the present invention include those described herein in the Examples section. The double-stranded nucleic acid molecule including both the coding strand having SEQ ID NO:19 and the complementary non-coding strand (the nucleic acid sequence of which can be readily determined by one skilled in the art and is shown herein as SEQ ID NO:21) is referred to herein as Fc<sub>ε</sub>R nucleic acid molecule ncFc<sub>ε</sub>Rα<sub>4991</sub>. Translation of SEQ ID NO:19 suggests that nucleic acid molecule ncFc<sub>ε</sub>Rα<sub>4991</sub> encodes a full-length Fc<sub>ε</sub>R α chain protein of about 253 amino acids, referred to herein as PcFc<sub>ε</sub>Rα<sub>4253</sub>, represented by SEQ ID NO:20, assuming an open reading frame having an initiation (start) codon spanning from about nucleotide 35 through about nucleotide 37 of SEQ ID NO:19 and the termination codon spans from about nucleotide 793 through about nucleotide 795 of SEQ ID NO:19. The coding region encoding PcFc<sub>ε</sub>Rα<sub>4253</sub>, excluding the stop codon, is represented by nucleic acid molecule ncFc<sub>ε</sub>Rα<sub>4759</sub>, having a coding strand with the nucleic acid sequence represented by SEQ ID NO:22 and a complementary strand with nucleic acid sequence SEQ ID NO:23. SEQ ID NO:19 encodes a signal peptide spanning from about amino acid 1 through about amino acid 24, as well as a mature protein of about 229 amino acids, denoted herein as PcFc<sub>ε</sub>Rα<sub>4229</sub>, the amino acid sequence of which is represented herein as SEQ ID NO:24. The nucleic acid molecule encoding the apparent mature protein is referred to as ncFc<sub>ε</sub>Rα<sub>4687</sub>, the nucleic acid sequence of the coding strand of which is denoted herein as SEQ ID NO:30. SEQ ID NO:19 also encodes a hydrophobic transmembrane domain which extends from about amino acid 172 to about amino acid 228 of SEQ ID NO:24. Knowledge of these nucleic

acid and amino acid sequences allows one skilled in the art to make modifications to the respective nucleic acid molecules and proteins to, for example, develop a canine  $Fc_\epsilon R \alpha$  chain protein with increased solubility and/or a truncated protein capable of detecting canine IgE, e.g.,  $PcFc_\epsilon R\alpha_{4_{197}}$ , spanning from about amino acid 1 to about amino acid 197 of SEQ ID NO:20, and having SEQ ID NO:28; or  $PcFc_\epsilon R\alpha_{4_{173}}$ , spanning from about amino acid 25 to about amino acid 197 of SEQ ID NO:20, and having SEQ ID NO:31.

Preferred  $Fc_\epsilon R$  molecules include  $PcFc_\epsilon R\alpha_{4_{253}}$ ,  $PcFc_\epsilon R\alpha_{4_{229}}$ ,  $PcFc_\epsilon R\alpha_{4_{197}}$ ,  $PcFc_\epsilon R\alpha_{4_{173}}$  and allelic variants thereof, as well as  $PcFc_\epsilon R\alpha_{1_{197}}$ ,  $PcFc_\epsilon R\alpha_{2_{197}}$ ,  $PcFc_\epsilon R\alpha_{3_{199}}$  (which are disclosed in the Examples section) and allelic variants thereof.

Preferred nucleic acid molecules to encode a  $Fc_\epsilon R$  molecules include  $ncFc_\epsilon R\alpha_{4_{591}}$ ,  $ncFc_\epsilon R\alpha_{4_{687}}$ ,  $ncFc_\epsilon R\alpha_{4_{991}}$ ,  $ncFc_\epsilon R\alpha_{4_{759}}$  and allelic variants thereof, as well as  $ncFc_\epsilon R\alpha_{1_{609}}$ ,  $ncFc_\epsilon R\alpha_{1_{591}}$ ,  $ncFc_\epsilon R\alpha_{2_{609}}$ ,  $ncFc_\epsilon R\alpha_{2_{591}}$ ,  $ncFc_\epsilon R\alpha_{3_{617}}$ ,  $ncFc_\epsilon R\alpha_{3_{597}}$  (which are disclosed in the Examples section) and allelic variants thereof. A preferred nucleic acid sequence encoding a canine  $Fc_\epsilon R$  molecule includes SEQ ID NO:3, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:16, SEQ ID NO:19, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:27, SEQ ID NO:30, and/or a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule comprising any of said nucleic acid sequences.

An isolated canine  $Fc_\epsilon R$  molecule protein of the present invention can be produced by culturing a cell capable of expressing the protein under conditions effective to produce the protein, and recovering the protein. A preferred cell to culture is a recombinant cell that is capable of expressing the protein, the recombinant cell being produced by transforming a host cell with one or more nucleic acid molecules of the present invention. Transformation of a nucleic acid molecule into a cell can be accomplished by any method by which a nucleic acid molecule can be inserted into the cell. Transformation techniques include, but are not limited to, transfection, electroporation, microinjection, lipofection, adsorption, and protoplast fusion. A recombinant cell may remain unicellular or may grow into a tissue, organ or a multicellular organism. Transformed nucleic acid molecules of the present invention can remain extrachromosomal or can integrate into one or more sites within a chromosome of the transformed (i.e., recombinant) cell in such a manner that their

ability to be expressed is retained. Suitable and preferred nucleic acid molecules with which to transform a cell are as disclosed herein for suitable and preferred  $Fc_\epsilon R$  nucleic acid molecules per se. Particularly preferred nucleic acid molecules to include in recombinant cells of the present invention include  $ncFc_\epsilon R\alpha 1_{609}$ ,  $ncFc_\epsilon R\alpha 1_{591}$ ,  
 5  $ncFc_\epsilon R\alpha 2_{609}$ ,  $ncFc_\epsilon R\alpha 2_{591}$ ,  $ncFc_\epsilon R\alpha 3_{617}$ ,  $ncFc_\epsilon R\alpha 3_{597}$ ,  $ncFc_\epsilon R\alpha 4_{591}$ ,  $ncFc_\epsilon R\alpha 4_{687}$ ,  
 $ncFc_\epsilon R\alpha 4_{991}$  and/or  $ncFc_\epsilon R\alpha 4_{759}$ .

Suitable host cells to transform include any cell that can be transformed with a nucleic acid molecule of the present invention. Host cells can be either untransformed cells or cells that are already transformed with at least one nucleic acid molecule. Host  
 10 cells of the present invention either can be endogenously (i.e., naturally) capable of producing a canine  $Fc_\epsilon R$  molecule protein of the present invention or can be capable of producing such proteins after being transformed with at least one nucleic acid molecule of the present invention. Host cells of the present invention can be any cell capable of producing at least one protein of the present invention, and include bacterial, fungal  
 15 (including yeast), parasite (including protozoa and ectoparasite), insect, other animal and plant cells.

Preferably, a recombinant cell is transfected with a recombinant molecule of the present invention. A recombinant molecule of the present invention includes at least one of any nucleic acid molecules heretofore described operatively linked to at least one of  
 20 any transcription control sequence capable of effectively regulating expression of the nucleic acid molecule(s) in the cell to be transformed, examples of which are disclosed herein. Particularly preferred recombinant molecules include  $pVL-ncFc_\epsilon R\alpha 4_{591}$ ,  $pVL-ncFc_\epsilon R\alpha 1_{609}$ ,  $pVL-ncFc_\epsilon R\alpha 2_{609}$ , and  $pVL-ncFc_\epsilon R\alpha 3_{617}$ . Details regarding the production of  $Fc_\epsilon R$  molecule nucleic acid molecule-containing recombinant molecules are disclosed  
 25 herein. Particularly preferred recombinant cells of the present invention include *S. frugiperda*: $pVL-ncFc_\epsilon R\alpha 4_{591}$ , *Trichoplusia ni*: $BV-ncFc_\epsilon R\alpha 4_{591}$ , *S. frugiperda*: $pVL-ncFc_\epsilon R\alpha 1_{609}$ , *S. frugiperda*: $pVL-ncFc_\epsilon R\alpha 2_{609}$ , *S. frugiperda*: $pVL-ncFc_\epsilon R\alpha 3_{608}$ ,  
*Trichoplusia ni*: $BV-ncFc_\epsilon R\alpha 1_{609}$ , *Trichoplusia ni*: $BV-ncFc_\epsilon R\alpha 2_{609}$ , and *Trichoplusia ni*: $BV-ncFc_\epsilon R\alpha 3_{617}$ .

30 A  $Fc_\epsilon R$  molecule of the present invention can include chimeric molecules comprising a portion of a  $Fc_\epsilon R$  molecule that binds to an IgE and a second molecule that



enables the chimeric molecule to be bound to a substrate in such a manner that the  $Fc_\epsilon R$  portion binds to IgE in essentially the same manner as a  $Fc_\epsilon R$  molecule that is not bound to a substrate. An example of a suitable second molecule includes a portion of an immunoglobulin molecule.

- 5 A canine  $Fc_\epsilon R$  molecule of the present invention can be contained in a formulation, herein referred to as a  $Fc_\epsilon R$  formulation. For example, a canine  $Fc_\epsilon R$  molecule can be combined with a buffer in which the  $Fc_\epsilon R$  is solubilized, and/or with a carrier. Suitable buffers and carriers are known to those skilled in the art. Examples of suitable buffers include any buffer in which a  $Fc_\epsilon R$  can function to selectively bind to
- 10 IgE, such as, but not limited to, phosphate buffered saline, water, saline, phosphate buffer, bicarbonate buffer, HEPES buffer (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid buffered saline), TES buffer (Tris-EDTA buffered saline), Tris buffer and TAE buffer (Tris-acetate-EDTA). Examples of carriers include, but are not limited to, polymeric matrices, toxoids, and serum albumins, such as bovine serum
- 15 albumin. Carriers can be combined with  $Fc_\epsilon R$  or conjugated (i.e., attached) to  $Fc_\epsilon R$  in such a manner as to not substantially interfere with the ability of the  $Fc_\epsilon R$  to selectively bind to IgE.

- A canine  $Fc_\epsilon R$  molecule of the present invention can be bound to the surface of a cell expressing the  $Fc_\epsilon R$ . A preferred  $Fc_\epsilon R$ -bearing cell includes a recombinant cell
- 20 expressing a nucleic acid molecule encoding a canine  $Fc_\epsilon R$  alpha chain of the present invention. A more preferred recombinant cell of the present invention expresses a nucleic acid molecule that encodes at least one of the following proteins:  $PcFc_\epsilon R\alpha 1_{197}$ ,  $PcFc_\epsilon R\alpha 2_{197}$ ,  $PcFc_\epsilon R\alpha 3_{199}$ ,  $PcFc_\epsilon R\alpha 4_{253}$ ,  $PcFc_\epsilon R\alpha 4_{229}$ ,  $PcFc_\epsilon R\alpha 4_{197}$  and  $PcFc_\epsilon R\alpha 4_{173}$ . An even more preferred recombinant cell expresses a nucleic acid molecule including
- 25  $ncFc_\epsilon R\alpha 1_{609}$ ,  $ncFc_\epsilon R\alpha 1_{591}$ ,  $ncFc_\epsilon R\alpha 2_{609}$ ,  $ncFc_\epsilon R\alpha 2_{591}$ ,  $ncFc_\epsilon R\alpha 3_{617}$ ,  $ncFc_\epsilon R\alpha 3_{597}$ ,  $ncFc_\epsilon R\alpha 4_{591}$ ,  $ncFc_\epsilon R\alpha 4_{687}$ ,  $ncFc_\epsilon R\alpha 4_{991}$  and  $ncFc_\epsilon R\alpha 4_{759}$ , or allelic variants thereof, with a recombinant cell expressing a nucleic acid molecule comprising a nucleic acid sequence SEQ ID NO:3, SEQ ID NO:8, SEQ ID NO:13 or SEQ ID NO:27, or a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule comprising SEQ
- 30 ID NO:3, SEQ ID NO:8, SEQ ID NO:13 or SEQ ID NO:27, being even more preferred.

In addition, a  $Fc_\epsilon R$  formulation of the present invention can include not only a  $Fc_\epsilon R$  but also one or more additional antigens or antibodies useful in detecting IgE. As used herein, an antigen refers to any molecule capable of being selectively bound by an antibody. As used herein, specific binding of a first molecule to a second molecule  
5 refers to the ability of the first molecule to preferentially bind to (e.g., have higher affinity higher avidity for) the second molecule when compared to the ability of a first molecule to bind to a third molecule. The first molecule need not necessarily be the natural ligand of the second molecule. Examples of antibodies used in the present invention include, but are not limited to, antibodies that bind selectively to the constant  
10 region of an IgE heavy chain (i.e., anti-IgE isotype antibodies) or antibodies that bind selectively to an IgE having a specific antigen specificity (i.e., anti-IgE idiotype antibodies). Examples of antigens used in the present invention include any antigen known to induce the production of IgE. Preferred antigens include allergens and parasite antigens. Allergens of the present invention are preferably derived from fungi, trees,  
15 weeds, shrubs, grasses, wheat, corn, soybeans, rice, eggs, milk, cheese, bovines (or cattle), poultry, swine, sheep, yeast, fleas, flies, mosquitos, mites, midges, biting gnats, lice, bees, wasps, ants, true bugs or ticks. A suitable flea allergen includes an allergen derived from a flea, and in particular a flea saliva antigen. Preferred flea saliva antigens include antigens such as those disclosed in PCT Patent Publication No. WO 96/11271,  
20 published April 18, 1996, by Frank et al. (this publication is incorporated by reference herein in its entirety), U.S. Patent Application Serial Nos. 08/319,590 (filed Oct. 7, 1994), 08/487,001 (filed June 7, 1995), 08/487,608 (filed June 7, 1995) and 08/630,822 (filed April 10, 1996), with flea saliva products and flea saliva proteins being particularly preferred. According to the present invention, a flea saliva protein includes  
25 a protein produced by recombinant DNA methods, as well as proteins isolated by other methods disclosed in PCT Patent Publication No. WO 96/11271, U.S. Patent Application Serial Nos. 08/319,590 (filed Oct. 7, 1994), 08/487,001 (filed June 7, 1995), 08/487,608 (filed June 7, 1995) and 08/630,822 (filed April 10, 1996).

Preferred general allergens include those derived from grass, Meadow Fescue,  
30 Curly Dock, plantain, Mexican Firebush, Lamb's Quarters, pigweed, ragweed, sage, elm, cocklebur, Box Elder, walnut, cottonwood, ash, birch, cedar, oak, mulberry, cockroach,

*Dermataphagoides*, *Alternaria*, *Aspergillus*, *Cladosporium*, *Fusarium*,  
*Helminthosporium*, *Mucor*, *Penicillium*, *Pullularia*, *Rhizopus* and/or *Tricophyton*. More  
preferred general allergens include those derived from Johnson Grass, Kentucky Blue  
Grass, Meadow Fescue, Orchard Grass, Perennial Rye Grass, Redtop Grass, Timothy  
5 Grass, Bermuda Grass, Brome Grass, Curly Dock, English Plantain, Mexican Firebush,  
Lamb's Quarters, Rough Pigweed Short Ragweed, Wormwood Sage, American Elm,  
Common Cocklebur, Box Elder, Black Walnut, Eastern Cottonwood, Green Ash, River  
Birch, Red Cedar, Red Oak, Red Mulberry, Cockroach, *Dermataphagoides farinae*,  
*Alternaria alternata*, *Aspergillus fumigatus*, *Cladosporium herbarum*, *Fusarium*  
10 *vasinfectum*, *Helminthosporium sativum*, *Mucor recemosus*, *Penicillium notatum*,  
*Pullularia pullulans*, *Rhizopus nigricans* and/or *Tricophyton* spp. Preferred parasite  
antigens include, but are not limited to, helminth antigens, in particular heartworm  
antigens, such as Di33 (described in U.S. Patent Application Serial No. 08/715,628, filed  
September 18, 1996, to Grievc et al.; this publication is incorporated by reference herein  
15 in its entirety). The term "derived from" refers to a natural allergen of such plants or  
organisms (i.e., an allergen directly isolated from such plants or organisms), as well as  
non-natural allergens of such plants or organisms that possess at least one epitope  
capable of eliciting an immune response against an allergen (e.g., produced using  
recombinant DNA technology or by chemical synthesis).

20 The present invention also includes canine  $Fc\epsilon R$  mimetopes and use thereof to  
detect IgE. In accordance with the present invention, a "mimetope" refers to any  
compound that is able to mimic the ability of a canine  $Fc\epsilon R$  molecule to bind to canine  
IgE. A mimetope can be a peptide that has been modified to decrease its susceptibility  
to degradation but that still retains IgE-binding activity. Other examples of mimetopes  
25 include, but are not limited to, carbohydrate-based compounds, lipid-based compounds,  
nucleic acid-based compounds, natural organic compounds, synthetically derived  
organic compounds, anti-idiotypic antibodies and/or catalytic antibodies, or fragments  
thereof. A mimetope can be obtained by, for example, screening libraries of synthetic  
compounds for compounds capable of binding to IgE. A mimetope can also be obtained  
30 by, for example, rational drug design. In a rational drug design procedure, the three-  
dimensional structure of a compound of the present invention can be analyzed by, for

example, nuclear magnetic resonance (NMR) or x-ray crystallography. The three-dimensional structure can then be used to predict structures of potential mimetopes by, for example, computer modeling. The predicted mimetope structures can then be produced by, for example, chemical synthesis, recombinant DNA technology, or by  
5 isolating a mimetope from a natural source. Specific examples of  $Fc_\epsilon R$  mimetopes include anti-idiotypic antibodies, oligonucleotides produced using Selex® technology, peptides identified by random screening of peptide libraries and proteins identified by phage display technology.

One embodiment of the present invention is a method to detect canine IgE which  
10 includes the steps of: (a) contacting an isolated canine  $Fc_\epsilon$  receptor ( $Fc_\epsilon R$ ) molecule with a putative canine IgE-containing composition under conditions suitable for formation of a  $Fc_\epsilon R$  molecule:IgE complex; and (b) detecting levels of IgE by detecting said  $Fc_\epsilon R$  molecule:IgE complex. Presence of such a  $Fc_\epsilon R$  molecule:IgE complex indicates that the canine is producing IgE. The present method can further include the step of  
15 determining whether a canine IgE complexed with a canine  $Fc_\epsilon R$  molecule is heat labile. Certain classes of IgE are heat labile when incubated at about 56°C for about 4 hours. Without being bound by theory, Applicants believe that heat labile forms of IgE bind to certain allergens and non-heat labile forms of IgE bind to other types of allergens. As such, detection of heat labile IgE compared with non-heat labile IgE can be used to  
20 discriminate between allergen sensitivities. For example, Applicants believe that canine IgE antibodies that bind to certain flea allergens and heartworm allergens are heat labile while canine IgE antibodies that bind to certain plant allergens are not heat labile. Thus, the presence of non-heat labile IgE can indicate that an animal is sensitive to certain plant allergens but not to certain flea or heartworm allergens. Moreover, Applicants  
25 believe that identification of heat labile IgE and non-heat labile IgE using a canine  $Fc_\epsilon R$  suggests the presence of different sub-populations of IgE that may or may not have substantially similar structures to known IgE. As such, a  $Fc_\epsilon R$  molecule of the present invention may be useful for detecting molecules bound by the  $Fc_\epsilon R$  molecule that are not identical to a known IgE.

As used herein, canine refers to any member of the dog family, including domestic dogs, wild dogs and zoo dogs. Examples of dogs include, but are not limited to, domestic dogs, wild dogs, foxes, wolves, jackals and coyotes.

As used herein, the term "contacting" refers to combining or mixing, in this case  
5 a putative IgE-containing composition with a canine Fc<sub>ε</sub>R molecule. Formation of a complex between a canine Fc<sub>ε</sub>R and a canine IgE refers to the ability of the Fc<sub>ε</sub>R to selectively bind to the IgE in order to form a stable complex that can be measured (i.e., detected). As used herein, the term selectively binds to an IgE refers to the ability of a Fc<sub>ε</sub>R of the present invention to preferentially bind to IgE, without being able to  
10 substantially bind to other antibody isotypes. Binding between a Fc<sub>ε</sub>R and an IgE is effected under conditions suitable to form a complex; such conditions (e.g., appropriate concentrations, buffers, temperatures, reaction times) as well as methods to optimize such conditions are known to those skilled in the art, and examples are disclosed herein. Examples of complex formation conditions are also disclosed in, for example, in  
15 Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press, 1989; the reference Sambrook et al., *ibid.*, is incorporated by reference herein in its entirety.

As used herein, the term "detecting complex formation" refers to determining if any complex is formed, i.e., assaying for the presence (i.e., existence) of a complex. If  
20 complexes are formed, the amount of complexes formed can, but need not be, determined. Complex formation, or selective binding, between canine Fc<sub>ε</sub>R and canine IgE in the composition can be measured (i.e., detected, determined) using a variety of methods standard in the art (see, for example, Sambrook et al. *ibid.*), examples of which are disclosed herein.

25 In one embodiment, a putative canine IgE-containing composition of the present method includes a biological sample from a caninc. A suitable biological sample includes, but is not limited to, a bodily fluid composition or a cellular composition. A bodily fluid refers to any fluid that can be collected (i.e., obtained) from an animal, examples of which include, but are not limited to, blood, serum, plasma, urine, tears,  
30 aqueous humor, central nervous system fluid (CNF), saliva, lymph, nasal secretions, milk and feces. Such a composition of the present method can, but need not be,

pretreated to remove at least some of the non-IgE isotypes of immunoglobulin and/or other proteins, such as albumin, present in the fluid. Such removal can include, but is not limited to, contacting the bodily fluid with a material, such as Protein G, to remove IgG antibodies and/or affinity purifying IgE antibodies from other components of the body fluid by exposing the fluid to, for example, Concanavalin A. In another embodiment, a composition includes collected bodily fluid that is pretreated to concentrate immunoglobulin contained in the fluid. For example, immunoglobulin contained in a bodily fluid can be precipitated from other proteins using ammonium sulfate. A preferred composition of the present method is serum.

10 In another embodiment, a composition of the present method includes an IgE-producing cell. Such a cell can have IgE bound to the surface of the cell and/or can secrete IgE. Examples of such cells include basophil cells and myeloma cells. IgE can be bound to the surface of a cell, for example by being either bound directly to the membrane of a cells or bound to a molecule (e.g., an antigen) bound to the surface of the cell.

15 A complex can be detected in a variety of ways including, but not limited to, use of one or more of the following assays: an enzyme-linked immunoassay, a radioimmunoassay, a fluorescence immunoassay, a chemiluminescent assay, a lateral flow assay, an agglutination assay, a particulate-based assay (e.g., using particulates such as, but not limited to, magnetic particles or plastic polymers, such as latex or polystyrene beads), an immunoprecipitation assay, a BioCore™ assay (e.g., using colloidal gold) and an immunoblotting assay (e.g., a western blot). Such assays are well known to those skilled in the art. Assays can be used to give qualitative or quantitative results depending on how they are used. Some assays, such as agglutination, particulate separation, and immunoprecipitation, can be observed visually (e.g., either by eye or by a machine, such as a densitometer or spectrophotometer) without the need for a detectable marker. In other assays, conjugation (i.e., attachment) of a detectable marker to the Fc<sub>ε</sub>R or to a reagent that selectively binds to the Fc<sub>ε</sub>R or to the IgE being detected (described in more detail below) aids in detecting complex formation. Examples of detectable markers include, but are not limited to, a radioactive label, a fluorescent label, a chemiluminescent label, a chromophoric label or a ligand. A ligand refers to a molecule

that binds selectively to another molecule. Preferred detectable markers include, but are not limited to, fluorescein, a radioisotope, a phosphatase (e.g., alkaline phosphatase), biotin, avidin, a peroxidase (e.g., horseradish peroxidase) and biotin-related compounds or avidin-related compounds (e.g., streptavidin or ImmunoPure® NeutrAvidin®).

- 5 Preferably, biotin is conjugated to an alpha chain of a  $Fc_\epsilon R$ . Preferably a carbohydrate group of the  $Fc_\epsilon R$  alpha chain is conjugated to biotin.

In one embodiment, a complex is detected by contacting a putative IgE-containing composition with a canine  $Fc_\epsilon R$  molecule that is conjugated to a detectable marker. A suitable detectable marker to conjugate to a  $Fc_\epsilon R$  molecule includes, but is  
10 not limited to, a radioactive label, a fluorescent label, a chemiluminescent label or a chromophoric label. A detectable marker is conjugated to a  $Fc_\epsilon R$  molecule or a reagent in such a manner as not to block the ability of the  $Fc_\epsilon R$  or reagent to bind to the IgE being detected. Preferably, a carbohydrate group of a  $Fc_\epsilon R$  is conjugated to biotin.

In another embodiment, a  $Fc_\epsilon R$  molecule:IgE complex is detected by contacting a  
15 putative IgE-containing composition with a  $Fc_\epsilon R$  molecule and then contacting the complex with an indicator molecule. Suitable indicator molecules of the present invention include molecules that can bind to either the  $Fc_\epsilon R$  molecule or to the IgE antibody. As such, an indicator molecule can comprise, for example, a  $Fc_\epsilon R$  molecule, an antigen, an antibody and a lectin, depending upon which portion of the  $Fc_\epsilon R$   
20 molecule:IgE complex is being detected. Preferred identifying labeled compounds that are antibodies include, for example, anti-IgE antibodies and anti- $Fc_\epsilon R$  antibodies. Preferred lectins include those lectins that bind to high-mannose groups. More preferred lectins bind to high-mannose groups present on a  $Fc_\epsilon R$  molecule of the present invention produced in insect cells. An indicator molecule itself can be attached to a detectable  
25 marker of the present invention. For example, an antibody can be conjugated to biotin, horseradish peroxidase, alkaline phosphatase or fluorescein.

In one preferred embodiment, a  $Fc_\epsilon R$  molecule:IgE complex is detected by contacting the complex with a reagent that selectively binds to a  $Fc_\epsilon R$  molecule of the present invention. Examples of such a reagent include, but are not limited to, an  
30 antibody that selectively binds to a  $Fc_\epsilon R$  molecule (referred to herein as an anti- $Fc_\epsilon R$  antibody) or a compound that selectively binds to a detectable marker conjugated to a

Fc<sub>ε</sub>R molecule. Fc<sub>ε</sub>R molecules conjugated to biotin are preferably detected using streptavidin, more preferably using ImmunoPure® NeutrAvidin® (available from Pierce, Rockford, IL).

In another preferred embodiment, a Fc<sub>ε</sub>R molecule:IgE complex is detected by contacting the complex with a reagent that selectively binds to an IgE antibody (referred to herein as an anti-IgE reagent). Examples of such an anti-IgE reagent include, but are not limited to, a secondary antibody that is an anti-isotype antibody (e.g., an antibody that selectively binds to the constant region of an IgE), an antibody-binding bacterial surface protein (e.g., Protein A or Protein G), an antibody-binding cell (e.g., a B cell, a T cell, a natural killer cell, a polymorphonuclear leukocyte cell, a monocyte cell or a macrophage cell), an antibody-binding eukaryotic cell surface protein (e.g., an Fc receptor), and an antibody-binding complement protein. Preferred anti-IgE reagents include, but are not limited to, D9 (provided by Doug DeBoer, University of Wisconsin), and CMI antibody #9, CMI antibody #19, CMI antibody #59 and CMI antibody #71 (available from Custom Monoclonal International, West Sacramento, CA). In particular, as used herein, an anti-IgE antibody includes not only a complete antibody but also any subunit or portion thereof that is capable of selectively binding to an IgE heavy chain constant region. For example, a portion of an anti-IgE reagent can include an Fab fragment or a F(ab')<sub>2</sub> fragment, which are described in detail in Janeway et al., in *Immunobiology, the Immune System in Health and Disease*, Garland Publishing, Inc., NY, 1996 (which is incorporated herein by this reference in its entirety).

In one embodiment a complex can be formed and detected in solution. In another embodiment, a complex can be formed in which one or more members of the complex are immobilized on (e.g., coated onto) a substrate. Immobilization techniques are known to those skilled in the art. Suitable substrate materials include, but are not limited to, plastic, glass, gel, celluloid, paper, PVDF (poly-vinylidene-fluoride), nylon, nitrocellulose, and particulate materials such as latex, polystyrene, nylon, nitrocellulose, agarose and magnetic resin. Suitable shapes for substrate material include, but are not limited to, a well (e.g., microtiter dish well), a plate, a dipstick, a bead, a lateral flow apparatus, a membrane, a filter, a tube, a dish, a celluloid-type matrix, a magnetic particle, and other particulates. A particularly preferred substrate comprises an ELISA



plate, a dipstick, a radioimmunoassay plate, agarose beads, plastic beads, latex beads, immunoblot membranes and immunoblot papers. In one embodiment, a substrate, such as a particulate, can include a detectable marker.

A preferred method to detect canine IgE is an immunosorbent assay. An  
5 immunoabsorbent assay of the present invention comprises a capture molecule and an indicator molecule. A capture molecule of the present invention binds to an IgE in such a manner that the IgE is immobilized to a substrate. As such, a capture molecule is preferably immobilized to a substrate of the present invention prior to exposure of the capture molecule to a putative IgE-containing composition. An indicator molecule of  
10 the present invention detects the presence of an IgE bound to a capture molecule. As such, an indicator molecule preferably is not immobilized to the same substrate as a capture molecule prior to exposure of the capture molecule to a putative IgE-containing composition.

A preferred immunoabsorbent assay method includes a step of either: (a) binding  
15 a canine  $Fc_\epsilon R$  molecule to a substrate prior to contacting a canine  $Fc_\epsilon R$  molecule with a putative IgE-containing composition to form a canine  $Fc_\epsilon R$  molecule-coated substrate; or (b) binding a putative canine IgE-containing composition to a substrate prior to contacting a canine  $Fc_\epsilon R$  molecule with a putative IgE-containing composition to form a putative IgE-containing composition-coated substrate. Preferably, the substrate is a non-  
20 coated substrate, an antigen-coated substrate or an anti-IgE antibody-coated substrate.

Both a capture molecule and an indicator molecule of the present invention are capable of binding to an IgE. Preferably, a capture molecule binds to a different region of an IgE than an indicator molecule, thereby allowing a capture molecule to be bound to an IgE at the same time as an indicator molecule. The use of a reagent as a capture  
25 molecule or an indicator molecule depends upon whether the molecule is immobilized to a substrate when the molecule is exposed to an IgE. For example, a canine  $Fc_\epsilon R$  molecule of the present invention is used as a capture molecule when the  $Fc_\epsilon R$  molecule is bound to a substrate. Alternatively, a canine  $Fc_\epsilon R$  molecule is used as an indicator molecule when the  $Fc_\epsilon R$  molecule is not bound to a substrate. Suitable molecules for  
30 use as capture molecules or indicator molecules include, but are not limited to, a canine

Fc<sub>ε</sub>R molecule of the present invention, an antigen reagent or an anti-IgE antibody reagent of the present invention.

An immunoabsorbent assay of the present invention can further comprise one or more layers and/or types of secondary molecules or other binding molecules capable of detecting the presence of an indicator molecule. For example, an untagged (i.e., not conjugated to a detectable marker) secondary antibody that selectively binds to an indicator molecule can be bound to a tagged (i.e., conjugated to a detectable marker) tertiary antibody that selectively binds to the secondary antibody. Suitable secondary antibodies, tertiary antibodies and other secondary or tertiary molecules can be selected by those of skill in the art. Preferred secondary molecules of the present invention include an antigen, an anti-IgE idiotype antibody and an anti-IgE isotypic antibody. Preferred tertiary molecules can be selected by a skilled artisan based upon the characteristics of the secondary molecule. The same strategy is applied for subsequent layers.

In one embodiment, a desired antigen is used as a capture molecule by being immobilized on a substrate, such as a microtiter dish well or a dipstick. Preferred antigens include those disclosed herein. A biological sample collected from an animal is applied to the substrate and incubated under conditions suitable (i.e., sufficient) to allow for antigen:IgE complex formation bound to the substrate (i.e., IgE in a sample binds to an antigen immobilized on a substrate). Excess non-bound material (i.e., material from the biological sample that has not bound to the antigen), if any, is removed from the substrate under conditions that retain antigen:IgE complex binding to the substrate. Preferred conditions are described generally in Sambrook et al., *ibid.* An indicator molecule that can selectively bind to an IgE bound to the antigen is added to the substrate and incubated to allow formation of a complex between the indicator molecule and the antigen:IgE complex. The indicator molecule can be conjugated to a detectable marker (preferably to an enzyme label, to a colorimetric label, to a fluorescent label, to a radioisotope, or to a ligand such as of the biotin or avidin family). Excess indicator molecule is removed, a developing agent is added if required, and the substrate is submitted to a detection device for analysis. A preferred indicator molecule for this

embodiment is a canine  $Fc_\epsilon R$  molecule, preferably conjugated to biotin, to a fluorescent label or to an enzyme label.

In one embodiment, a canine  $Fc_\epsilon R$  molecule is used as a capture molecule by being immobilized on a substrate, such as a microtiter dish well or a dipstick. A  
5 biological sample collected from an animal is applied to the substrate and incubated under conditions suitable to allow for  $Fc_\epsilon R$  molecule:IgE complex formation bound to the substrate. Excess non-bound material, if any, is removed from the substrate under conditions that retain  $Fc_\epsilon R$  molecule:IgE complex binding to the substrate. An indicator molecule that can selectively bind to an IgE bound to the  $Fc_\epsilon R$  is added to the substrate  
10 and incubated to allow formation of a complex between the indicator molecule and the  $Fc_\epsilon R$  molecule:IgE complex. Preferably, the indicator molecule is conjugated to a detectable marker, preferably to an enzyme label, to a colorimetric label, to a fluorescent label, to a radioisotope, or to a ligand such as of the biotin or avidin family. Excess indicator molecule is removed, a developing agent is added if required, and the substrate  
15 is submitted to a detection device for analysis. A preferred indicator molecule for this embodiment is an antigen that will bind to IgE in the biological sample or an anti-IgE isotype or idiotype antibody, either preferably being conjugated to fluorescein, an enzyme or biotin.

In one embodiment, an anti-IgE antibody (e.g., isotype- or idiotype-specific  
20 antibody) is used as a capture molecule by being immobilized on a substrate, such as a microtiter dish well or a dipstick. A biological sample collected from a canine is applied to the substrate and incubated under conditions suitable to allow for anti-IgE antibody:IgE complex formation bound to the substrate. Excess non-bound material, if any, is removed from the substrate under conditions that retain anti-IgE antibody:IgE  
25 complex binding to the substrate. A canine  $Fc_\epsilon R$  molecule is added to the substrate and incubated to allow formation of a complex between the canine  $Fc_\epsilon R$  molecule and the anti-IgE antibody:IgE complex. Preferably, the canine  $Fc_\epsilon R$  molecule is conjugated to a detectable marker (preferably to biotin, an enzyme label or a fluorescent label). Excess  $Fc_\epsilon R$  molecule is removed, a developing agent is added if required, and the substrate is  
30 submitted to a detection device for analysis.

In one embodiment, an immunosorbent assay of the present invention does not utilize a capture molecule. In this embodiment, a biological sample collected from a canine is applied to a substrate, such as a microtiter dish well or a dipstick, and incubated under conditions suitable to allow for IgE binding to the substrate. Any IgE  
5 present in the bodily fluid is immobilized on the substrate. Excess non-bound material, if any, is removed from the substrate under conditions that retain IgE binding to the substrate. A canine  $Fc_\epsilon R$  molecule is added to the substrate and incubated to allow formation of a complex between the canine  $Fc_\epsilon R$  molecule and canine IgE. Preferably, the  $Fc_\epsilon R$  molecule is conjugated to a detectable marker (preferably to biotin, an enzyme  
10 label or a fluorescent label). Excess  $Fc_\epsilon R$  molecule is removed, a developing agent is added if required, and the substrate is submitted to a detection device for analysis.

Another preferred method to detect canine IgE is a lateral flow assay, examples of which are disclosed in U.S. Patent No. 5,424,193, issued June 13, 1995, by Pronovost et al.; U.S. Patent No. 5,415,994, issued May 16, 1995, by Imrich et al; WO 94/29696,  
15 published December 22, 1994, by Miller et al.; and WO 94/01775, published January 20, 1994, by Pawlak et al.; each of these patent publications is incorporated by reference herein in its entirety. In one embodiment, a biological sample is placed in a lateral flow apparatus that includes the following components: (a) a support structure defining a flow path; (b) a labeling reagent comprising a bead conjugated to an antigen, the labeling  
20 reagent being impregnated within the support structure in a labeling zone; and (c) a capture reagent comprising a canine IgE-binding composition. Preferred antigens include those disclosed herein. The capture reagent is located downstream of the labeling reagent within a capture zone fluidly connected to the labeling zone in such a manner that the labeling reagent can flow from the labeling zone into the capture zone.  
25 The support structure comprises a material that does not impede the flow of the beads from the labeling zone to the capture zone. Suitable materials for use as a support structure include ionic (i.e., anionic or cationic) material. Examples of such a material include, but are not limited to, nitrocellulose (NC), PVDF and carboxymethylcellulose (CM). The support structure defines a flow path that is lateral and is divided into zones,  
30 namely a labeling zone and a capture zone. The apparatus can further comprise a sample receiving zone located along the flow path, more preferably upstream of the labeling

reagent. The flow path in the support structure is created by contacting a portion of the support structure downstream of the capture zone, preferably at the end of the flow path, to an absorbent capable of absorbing excess liquid from the labeling and capture zones.

In this embodiment, the biological sample is applied to the sample receiving zone  
5 which includes a portion of the support structure. The labeling zone receives the sample from the sample receiving zone which is directed downstream by the flow path. The labeling zone comprises the labeling reagent that binds to IgE. A preferred labeling reagent is an antigen conjugated, either directly or through a linker, to a plastic bead substrate, such as to a latex bead. The substrate also includes a detectable marker,  
10 preferably a colorimetric marker. Typically, the labeling reagent is impregnated to the support structure by drying or lyophilization. The sample structure also comprises a capture zone downstream of the labeling zone. The capture zone receives labeling reagent from the labeling zone which is directed downstream by the flow path. The capture zone contains the capture reagent, preferably a canine  $Fc\epsilon R$  molecule of the  
15 present invention that immobilizes canine IgE complexed to the antigen in the capture zone. The capture reagent is preferably fixed to the support structure by drying or lyophilization. The labeling reagent accumulates in the capture zone and the accumulation is assessed visually or by an optical detection device.

In another embodiment, a lateral flow apparatus used to detect canine IgE  
20 includes: (a) a support structure defining a flow path; (b) a labeling reagent comprising a canine  $Fc\epsilon R$  molecule of the present invention, the labeling reagent impregnated within the support structure in a labeling zone; and (c) a capture reagent comprising an antigen, the capture reagent being located downstream of the labeling reagent within a capture zone fluidly connected to the labeling zone in such a manner that the labeling reagent  
25 can flow from the labeling zone into the capture zone. The apparatus preferably also includes a sample receiving zone located along the flow path, preferably upstream of the labeling reagent. The apparatus preferably also includes an absorbent located at the end of the flow path.

One embodiment of the present invention is an inhibition assay in which the  
30 presence of canine IgE in a putative canine IgE-containing composition is determined by adding such composition to a canine  $Fc\epsilon R$  molecule of the present invention and an

isolated canine IgE known to bind to the  $Fc_\epsilon R$  molecule. The absence of binding of the  $Fc_\epsilon R$  molecule to the known IgE indicating the presence of IgE in the putative IgE-containing composition.

The present invention also includes kits to detect canine IgE based, for example, on the disclosed detection methods. One embodiment is a kit to detect canine IgE comprising a canine  $Fc_\epsilon$  receptor ( $Fc_\epsilon R$ ) molecule and a means for detecting a canine IgE. Suitable and preferred canine  $Fc_\epsilon R$  molecules are disclosed herein. Suitable means of detection include compounds disclosed herein that bind to either the canine  $Fc_\epsilon R$  molecule or to a canine IgE. A preferred kit of the present invention further comprises a detection means including one or more antigens such as those disclosed herein, an antibody capable of selectively binding to canine IgE such as those disclosed herein and/or a compound capable of binding to a detectable marker conjugated to a canine  $Fc_\epsilon R$  molecule (e.g., avidin, streptavidin and ImmunoPure® NeutrAvidin when the detectable marker is biotin).

A preferred embodiment of a kit of the present invention is a flea allergen kit comprising a flea allergen such as those disclosed herein. A particularly preferred flea allergen for use with a flea allergen kit includes a flea saliva product or a flea saliva protein.

Another preferred kit of the present invention is a general allergen kit comprising an allergen common to all regions of the United States and a canine  $Fc_\epsilon R$  molecule of the present invention. As used herein, a "general allergen" kit refers to a kit comprising allergens that are found substantially throughout the United States (i.e., essentially not limited to certain regions of the United States). A general allergen kit provides an advantage over regional allergen kits because a single kit can be used to test a canid from any geographical location in the United States. Suitable and preferred general allergens for use with a general allergen kit of the present invention include those general allergens disclosed herein.

Another preferred kit of the present invention is a food allergen kit comprising (a) a food allergen such as beef, chicken, pork, a mixture of fish, such as cod, halibut or and tuna, egg, milk, Brewer's yeast, whole wheat, corn, soybean, cheese and/or rice, and

(b) a canine FcεR molecule of the present invention. Preferably, the beef, chicken, pork, fish, corn and rice, are cooked.

A preferred kit of the present invention is one in which the allergen is immobilized to a substrate. If a kit comprises two or more antigens, the kit can comprise one or more compositions, each composition comprising one antigen. As such, each antigen can be tested separately. A kit can also contain two or more diagnostic reagents for detecting canine IgE, additional isolated canine IgE antigens and/or antibodies as disclosed herein. Particularly preferred are kits used in a lateral flow assay format. It is within the scope of the present invention that a lateral flow assay kit can include one or more lateral flow assay apparatuses. Multiple lateral flow apparatuses can be attached to each other at one end of each apparatus, thereby creating a fan-like structure.

In particular, a method and kit of the present invention are useful for diagnosing abnormal conditions in animals that are associated with changing levels of canine IgE. Particularly preferred conditions to diagnose include allergies, parasitic infections and neoplasia. For example, a method and kit of the present invention are particularly useful for detecting flea allergy dermatitis (FAD), when such method or kit includes the use of a flea saliva antigen. FAD is defined as a hypersensitive response to fleabites. Preferably, a putative IgE-containing composition is obtained from an animal suspected of having FAD. In addition, methods and kits of the present invention are particularly useful for detecting helminth infection, in particular heartworm infection, when such methods or kits include the use of a helminth antigen, such as Di33. Preferably, a putative canine IgE-containing composition is obtained from a canine suspected of having a helminth infection.

The following examples are provided for the purposes of illustration and are not intended to limit the scope of the present invention.

#### EXAMPLES

It is to be noted that the Examples include a number of molecular biology, microbiology, immunology and biochemistry techniques considered to be known to those skilled in the art. Disclosure of such techniques can be found, for example, in Sambrook et al., *ibid.*, and related references.

Example 1

This example describes the construction of recombinant baculoviruses expressing a truncated portion of the  $\alpha$  chain of canine  $Fc_\epsilon$  receptor.

Recombinant molecules pVL-ncFc $_\epsilon$ R $\alpha$ 1<sub>609</sub>, pVL-ncFc $_\epsilon$ R $\alpha$ 2<sub>609</sub>, and pVL-ncFc $_\epsilon$ R $\alpha$ 3<sub>617</sub>, each containing nucleic acid molecules encoding the extracellular domain of the canine Fc $_\epsilon$ R  $\alpha$  chain, operatively linked to baculovirus polyhedron transcription control sequences were produced in the following manner. Three different canine Fc $_\epsilon$ R  $\alpha$  chain extracellular domain nucleic acid molecule-containing fragments, each of about 608 to about 609 nucleotides were amplified by polymerase chain reaction (PCR) from either a canine splenic mononuclear cell cDNA library or a canine lymph node mononuclear cell cDNA library, each library produced using standard techniques, using a forward primer CIERMet containing a *Bam*HI site, having the nucleic acid sequence 5'-TGC GGA TCC AAT ATG CCT GCT TCC ATG GGA G-3' (denoted SEQ ID NO:1) and a reverse primer CIERSec containing an *Eco*RI site, having the nucleic acid sequence 5'-TTG GAA TTC TTA CTC TTT TTT CAC AAT AAT GTT G-3' (denoted herein as SEQ ID NO:2). The resulting PCR products were digested with *Bam*HI and *Eco*RI to produce the following nucleic acid molecules: ncFc $_\epsilon$ R $\alpha$ 1<sub>609</sub> (also denoted ncFc $_\epsilon$ R $\alpha$ LN4<sub>609</sub>), ncFc $_\epsilon$ R $\alpha$ 2<sub>609</sub> (also denoted ncFc $_\epsilon$ R $\alpha$ SPL6<sub>609</sub>) and ncFc $_\epsilon$ R $\alpha$ 3<sub>617</sub> (also denoted ncFc $_\epsilon$ R $\alpha$ SPL3R<sub>617</sub>). Nucleic acid molecule ncFc $_\epsilon$ R $\alpha$ 1<sub>609</sub> was obtained from the PCR reaction derived from the canine lymph node mononuclear cell cDNA library. Nucleic acid molecules ncFc $_\epsilon$ R $\alpha$ 2<sub>609</sub> and ncFc $_\epsilon$ R $\alpha$ 3<sub>617</sub> were obtained from the PCR reaction derived from the canine splenic mononuclear cell cDNA library. Nucleic acid molecules ncFc $_\epsilon$ R $\alpha$ 1<sub>609</sub>, ncFc $_\epsilon$ R $\alpha$ 2<sub>609</sub>, and ncFc $_\epsilon$ R $\alpha$ 3<sub>617</sub> each were sequenced by the Sanger dideoxy chain termination method, using the PRISM<sup>TM</sup> Ready Dye Terminator Cycle Sequencing Kit with Ampli Taq DNA Polymerase, FS (available from the Perkin-Elmer Corporation, Norwalk, CT). Nucleic acid molecules ncFc $_\epsilon$ R $\alpha$ 1<sub>609</sub>, ncFc $_\epsilon$ R $\alpha$ 2<sub>609</sub>, and ncFc $_\epsilon$ R $\alpha$ 3<sub>617</sub> each contained an about 608 to an about 609 nucleotide fragment encoding the extracellular domain of the canine Fc $_\epsilon$ R  $\alpha$  chain, the coding strands of which have nucleic acid sequences denoted SEQ ID NO:3, SEQ ID NO:8, and SEQ ID NO:13, respectively. The complement of SEQ ID NO:3 is represented herein by SEQ



ID NO:5. The complement of SEQ ID NO:8 is represented herein by SEQ ID NO:10.  
The complement of SEQ ID NO:13 is represented herein by SEQ ID NO:15.

Translation of SEQ ID NO:3 indicates that nucleic acid molecule ncFc<sub>ε</sub>Rα1<sub>609</sub> encodes a Fc<sub>ε</sub>R protein of about 197 amino acids, referred to herein as PcFc<sub>ε</sub>Rα1<sub>197</sub>,  
5 having amino acid sequence SEQ ID NO:4, assuming an open reading frame having a start codon spanning from about nucleotide 10 through about nucleotide 12 of SEQ ID NO:3 and a stop codon spanning from about nucleotide 601 through about nucleotide 603 of SEQ ID NO:3. This open reading frame, excluding the stop codon, comprises nucleic acid molecule ncFc<sub>ε</sub>Rα1<sub>591</sub> of the present invention, the nucleic acid sequence of  
10 which is represented herein by SEQ ID NO:6. The complement of SEQ ID NO:6 is represented herein by SEQ ID NO:7.

Translation of SEQ ID NO:8 indicates that nucleic acid molecule ncFc<sub>ε</sub>Rα2<sub>609</sub> encodes a Fc<sub>ε</sub>R protein of about 197 amino acids, referred to herein as PcFc<sub>ε</sub>Rα2<sub>197</sub>,  
having amino acid sequence SEQ ID NO:9, assuming an open reading frame having a  
15 start codon spanning from about nucleotide 10 through about nucleotide 12 of SEQ ID NO:8 and a stop codon spanning from about nucleotide 601 through about nucleotide 603 of SEQ ID NO:8. This open reading frame, excluding the stop codon, comprises nucleic acid molecule ncFc<sub>ε</sub>Rα2<sub>591</sub> of the present invention, the nucleic acid sequence of which is represented herein by SEQ ID NO:11. The complement of SEQ ID NO:11 is  
20 represented herein by SEQ ID NO:12.

Translation of SEQ ID NO:13 indicates that nucleic acid molecule ncFc<sub>ε</sub>Rα3<sub>617</sub> encodes a Fc<sub>ε</sub>R protein of about 199 amino acids, referred to herein as PcFc<sub>ε</sub>Rα3<sub>199</sub>,  
having amino acid sequence SEQ ID NO:14, assuming that the initiation codon spans from about nucleotide 10 through about nucleotide 12 of SEQ ID NO:13 and the last  
25 codon spans from about nucleotide 595 through about nucleotide 597 of SEQ ID NO:13. This open reading frame comprises nucleic acid molecule ncFc<sub>ε</sub>Rα3<sub>597</sub> of the present invention, the nucleic acid sequence of which is represented herein by SEQ ID NO:16. The complement of SEQ ID NO:16 is represented herein by SEQ ID NO:17.

In order to produce baculovirus recombinant molecules capable of directing the  
30 production of PcFc<sub>ε</sub>Rα1<sub>197</sub>, PcFc<sub>ε</sub>Rα2<sub>197</sub>, and PcFc<sub>ε</sub>Rα3<sub>199</sub>, nucleic acid molecules ncFc<sub>ε</sub>Rα1<sub>609</sub>, ncFc<sub>ε</sub>Rα2<sub>609</sub>, and ncFc<sub>ε</sub>Rα3<sub>617</sub> were subcloned into unique *Bam*HI and

*Eco*RI sites of pVL1393 baculovirus shuttle plasmid (available from Pharmingen, San Diego, CA) to produce recombinant molecules referred to herein as pVL-ncFc<sub>ε</sub>Rα1<sub>609</sub>, pVL-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and pVL-ncFc<sub>ε</sub>Rα3<sub>617</sub>, respectively. The resultant recombinant molecules pVL-ncFc<sub>ε</sub>Rα1<sub>609</sub>, pVL-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and pVL-ncFc<sub>ε</sub>Rα3<sub>617</sub> were verified for proper insert orientation by restriction mapping.

Recombinant molecules pVL-ncFc<sub>ε</sub>Rα1<sub>609</sub>, pVL-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and pVL-ncFc<sub>ε</sub>Rα3<sub>617</sub> were co-transfected with a linear Baculogold™ baculovirus DNA (available from Pharmingen) into *S. frugiperda* Sf9 cells (available from Invitrogen Corp., San Diego, CA) using methods prescribed by the manufacturer to form recombinant cells *S. frugiperda*:pVL-ncFc<sub>ε</sub>Rα1<sub>609</sub>, *S. frugiperda*:pVL-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and *S. frugiperda*:pVL-ncFc<sub>ε</sub>Rα3<sub>617</sub>. Recombinant baculoviruses were plaque purified and amplified from each transfection by methods well known to those skilled in the art, to produce recombinant baculoviruses BV-ncFc<sub>ε</sub>Rα1<sub>609</sub>, BV-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and BV-ncFc<sub>ε</sub>Rα3<sub>617</sub>, respectively.

#### Example 2

This example describes the production of PcFc<sub>ε</sub>Rα1<sub>197</sub>, PcFc<sub>ε</sub>Rα2<sub>197</sub>, and PcFc<sub>ε</sub>Rα3<sub>199</sub> canine Fc<sub>ε</sub>R α chain proteins.

About 1.5 liter cultures of serum-free ex-Cell Medium (available from Invitrogen) were seeded with about  $1 \times 10^6$  *Trichoplusia ni* cells (High Five™ cells; available from Invitrogen) per milliliters (ml) of medium. The cell cultures were inoculated with recombinant baculoviruses BV-ncFc<sub>ε</sub>Rα1<sub>609</sub>, BV-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and BV-ncFc<sub>ε</sub>Rα3<sub>617</sub>, respectively, at multiplicities of infection (MOI) of about 2 to about 5 plaque forming units (pfu) per cell to produce recombinant cells *Trichoplusia ni*-BV-ncFc<sub>ε</sub>Rα1<sub>609</sub>, *Trichoplusia ni*-BV-ncFc<sub>ε</sub>Rα2<sub>609</sub>, and *Trichoplusia ni*-BV-ncFc<sub>ε</sub>Rα3<sub>617</sub>. The infections were allowed to proceed at a controlled temperature of 27°C for 48 hours, to produce recombinant proteins of PcFc<sub>ε</sub>Rα1<sub>197</sub>, PcFc<sub>ε</sub>Rα2<sub>197</sub>, and PcFc<sub>ε</sub>Rα3<sub>199</sub>. Following infection, cells were separated from the medium by centrifugation, and the medium was frozen at -70°C.

#### Example 3

This example describes the binding of PcFc<sub>ε</sub>Rα1<sub>197</sub>, PcFc<sub>ε</sub>Rα2<sub>197</sub>, or PcFc<sub>ε</sub>Rα3<sub>199</sub> protein to canine IgE.

About 4.5 ml of the culture media described immediately above containing PcFc<sub>c</sub>R $\alpha$ 1<sub>197</sub>, PcFc<sub>c</sub>R $\alpha$ 2<sub>197</sub>, or PcFc<sub>c</sub>R $\alpha$ 3<sub>199</sub>, respectively, were loaded onto columns comprising a canine IgE monoclonal antibody (a gift from Chris Grant, Custom Monoclonals International, West Sacramento, CA) linked to sepharose 4B. Each  
5 column was washed with about 4 ml of carbonate buffer (0.1 M NaHCO<sub>3</sub>, pH 8.3 and 0.5 M NaCl). Protein bound to the IgE on each column was eluted from the column using about 3 ml of 0.1 M glycine-HCl, pH 2.8. Each column was further washed with about 1 ml of carbonate buffer and then with about 4 ml of buffer comprising 0.1 M NaHCO<sub>3</sub>, pH 8.3. The elution samples and wash samples from a given column were  
10 combined and concentrated to a volume of about 0.35 ml. The eluted protein from each column was resolved on separate 14% Tris-glycine polyacrylamide-SDS gels. The gels were then stained with coomassie stain. A diffused band was observed at about 31 kilodaltons (kD).

Amino (N-) terminal amino acid sequencing analysis was performed on protein  
15 contained in the diffused band using standard procedures known to those in the art (see, for example, Geisow et al., 1989, in *Protein Sequencing: A Practical Approach*, JBC Findlay and MJ Geisow (eds.), IRL Press, Oxford, England, pp. 85-98; Hewick et al., 1981, *J. Biol. Chem.*, Vol. 256, pp. 7990-7997). The N-terminal partial amino acid sequence of a protein contained in the band was determined to be S D T L K P T V X M  
20 N P P X N L I (as represented in standard single letter code, and denoted herein as SEQ ID NO:18; "X" represents any amino acid). Comparison of SEQ ID NO:18 and the amino acid sequence of the canine Fc<sub>c</sub>R  $\alpha$  chain reported in Hayashi et al., *ibid.*, indicated that PcFc<sub>c</sub>R $\alpha$ 1<sub>197</sub>, PcFc<sub>c</sub>R $\alpha$ 2<sub>197</sub>, and PcFc<sub>c</sub>R $\alpha$ 3<sub>199</sub>, expressed in baculovirus, each bound to canine IgE antibodies.

#### 25 Example 4

This example describes the isolation, by DNA hybridization, and sequencing of a nucleic acid molecule encoding the Fc<sub>c</sub>R  $\alpha$  chain from *Canis canis*.

##### A. Isolation of nucleic acid molecule ncFc<sub>c</sub>R $\alpha$ 4<sub>991</sub>

A nucleic acid molecule was isolated from a canine mast cell cDNA library by  
30 the molecule's ability to hybridize with a <sup>32</sup>P-labeled probe derived from a PCR clone encoding the canine Fc<sub>c</sub>R  $\alpha$  chain. The canine mast cell cDNA library was prepared

using standard techniques. Using a modification of the protocol described in the cDNA Synthesis Kit, the mast cell cDNA library was screened, using duplicate plaque lifts, with a  $^{32}\text{P}$ -labeled probe comprising ncFc $_{\epsilon}$ R $\alpha$ 1 $_{609}$  (SEQ ID NO:3). A plaque purified clone containing a canine nucleic acid molecule encoding the Fc $_{\epsilon}$ R  $\alpha$  chain was  
5 converted into a double stranded recombinant molecule, using the ExAssist<sup>TM</sup> helper phage and SOLR<sup>TM</sup> *E. coli* according to the *in vivo* excision protocol described in the ZAP-cDNA Synthesis Kit (available from Stratagene). Double-stranded plasmid DNA was prepared using an alkaline lysis protocol, such as that described in Sambrook et al., *ibid.* The plasmid comprised a canine Fc $_{\epsilon}$ R  $\alpha$  chain nucleic acid molecule of about 991  
10 nucleotides denoted herein as ncFc $_{\epsilon}$ R $\alpha$ 4 $_{991}$ .

B. Sequence analysis of nucleic acid molecule ncFc $_{\epsilon}$ R $\alpha$ 4 $_{991}$

The nucleic acid molecule ncFc $_{\epsilon}$ R $\alpha$ 4 $_{991}$  was sequenced by standard Sanger dideoxy chain termination sequencing techniques (see, for example, Sambrook et al., *ibid.*). DNA sequence analysis, including the compilation of sequences and the  
15 determination of open reading frames, were performed using the MacVector<sup>TM</sup> program (available from the Eastman Kodak Company, New Haven, CT), or the DNAsis<sup>TM</sup> program (available from Hitachi Software, San Bruno, CA). Protein sequence analysis, including the determination of molecular weight and isoelectric point (pI) was performed using the MacVector<sup>TM</sup> program.

20 The nucleic acid sequence of the coding strand of ncFc $_{\epsilon}$ R $\alpha$ 4 $_{991}$  is denoted herein as SEQ ID NO:19. Translation of SEQ ID NO:19 suggests that nucleic acid molecule ncFc $_{\epsilon}$ R $\alpha$ 4 $_{991}$  encodes a full-length canine Fc $_{\epsilon}$ R  $\alpha$  chain protein of about 253 amino acids, referred to herein as PcFc $_{\epsilon}$ R $\alpha$ 4 $_{253}$ , having amino acid sequence SEQ ID NO:20, assuming an open reading frame in which the initiation codon spans from about  
25 nucleotide 35 through about nucleotide 37 of SEQ ID NO:19 and the termination codon spans from about nucleotide 794 through about nucleotide 796 of SEQ ID NO:19. The complement of SEQ ID NO:20 is represented herein by SEQ ID NO:21. The coding region encoding PcFc $_{\epsilon}$ R $\alpha$ 4 $_{253}$ , is represented by nucleic acid molecule ncFc $_{\epsilon}$ R $\alpha$ 4 $_{759}$ , having a coding strand with the nucleic acid sequence represented by SEQ ID NO:22  
30 and a complementary strand with nucleic acid sequence SEQ ID NO:23. The amino acid

sequence of PcFc<sub>ε</sub>Rα<sub>253</sub> (i.e., SEQ ID NO:21) predicts that PcFc<sub>ε</sub>Rα<sub>253</sub> has an estimated molecular weight of about 28.5 kD and an estimated pI of about 9.62.

Analysis of SEQ ID NO: 20 suggests the presence of a signal peptide encoded by a stretch of amino acids spanning from about amino acid 1 through about amino acid 24.

5 The proposed mature protein, denoted herein as PcFc<sub>ε</sub>Rα<sub>4229</sub>, contains about 229 amino acids, the sequence of which is shown as SEQ ID NO:24. The coding strand encoding PcFc<sub>ε</sub>Rα<sub>4229</sub> is represented herein as SEQ ID NO:30. The amino acid sequence of PcFc<sub>ε</sub>Rα<sub>4229</sub> (i.e., SEQ ID NO:24) predicts that PcFc<sub>ε</sub>Rα<sub>4229</sub> has an estimated molecular weight of about 26 kD, an estimated pI of about 9.65 and five predicted asparagine-  
10 linked glycosylation sites extending from about amino acids 29-31, 42-44, 71-73, 135-137 and 148-150, respectively.

Comparison of amino acid sequence SEQ ID NO:20 with amino acid sequences reported in GenBank indicates that SEQ ID NO:20 showed the most homology, i.e., about 100% identity between SEQ ID NO:20 and a *Canis canis* Fc<sub>ε</sub>R α chain protein  
15 (GenBank accession number D16413). Comparison of amino acid sequence SEQ ID NO:22 with nucleic acid sequences reported in GenBank indicates that SEQ ID NO:22 showed the most homology, i.e., about 100% identity between SEQ ID NO:22 and a canine mRNA for Fc<sub>ε</sub>R α chain (GenBank accession D16413).

#### Example 5

20 This Example demonstrates the production of secreted canine Fc<sub>ε</sub>R α chain protein in eukaryotic cells.

To produce a secreted form of a canine Fc<sub>ε</sub>R α chain, recombinant molecule pVL-ncFc<sub>ε</sub>Rα<sub>4391</sub>, containing a canine Fc<sub>ε</sub>R α chain nucleic acid molecule encoding a secreted form of canine Fc<sub>ε</sub>R α chain spanning nucleotides from about 35 through about  
25 625 of SEQ ID NO:19 operatively linked to baculovirus polyhedron transcription control sequences, was produced in the following manner. A canine Fc<sub>ε</sub>R α chain nucleic acid molecule of about 591 nucleotides was PCR amplified from ncFc<sub>ε</sub>Rα<sub>4991</sub> DNA using a sense primer canIgEr FWD having the nucleic acid sequence 5' GCG AAG ATC TAT AAA TAT GCC TGC TTC CAT GGG- 3' (SEQ ID NO:25; *Bgl*III site shown in bold)  
30 and an antisense primer canIgEr REV having the nucleic acid sequence 5' GCA GGA ATT CTT ACT CTT TTT TCA CAA TAA TGT -3' (SEQ ID NO:26; *Eco*RI site shown

in bold). The N-terminal primer was designed from the pol h sequence of baculovirus with modifications to enhance expression in the baculovirus system.

The about 591 base pair PCR product (referred to as ncFc<sub>c</sub>Rα<sub>4,591</sub>) has a coding strand nucleic acid sequence denoted herein as SEQ ID NO:27. The complement of  
5 SEQ ID NO:27 is represented herein by SEQ ID NO:29. Translation of SEQ ID NO:27 indicates that nucleic acid molecule ncFc<sub>c</sub>Rα<sub>4,591</sub> encodes a Fc<sub>c</sub>R α chain protein of about 197 amino acids, referred to herein as PcFc<sub>c</sub>Rα<sub>4,197</sub>, having amino acid sequence SEQ ID NO:28. Nucleic acid molecule ncFc<sub>c</sub>Rα<sub>591</sub> encodes a secretable form of the canine Fc<sub>c</sub>R α chain. The processed protein product encoded by ncFc<sub>c</sub>Rα<sub>4,591</sub> does not  
10 possess a leader sequence or transmembrane domain, and is referred to herein as PcFc<sub>c</sub>Rα<sub>4,173</sub>, represented herein by SEQ ID NO:31.

Nucleic acid molecule Bv-ncFc<sub>c</sub>Rα<sub>591</sub> was digested with *Bgl*III and *Eco*RI and subcloned into the unique *Bgl*III and *Eco*RI sites of baculovirus shuttle plasmid pVL1392 (available from Pharmingen, San Diego, CA) to produce the recombinant molecule  
15 referred to herein as pVL-ncFc<sub>c</sub>Rα<sub>591</sub>. The resultant recombinant molecule, pVL-ncFc<sub>c</sub>Rα<sub>591</sub>, was verified for proper insert orientation by restriction mapping. The recombinant molecule pVL-ncFc<sub>c</sub>Rα<sub>591</sub> was co-transfected with a Baculogold™ baculovirus DNA into *S. frugiperda* Sf9 cells (available from Invitrogen) to form recombinant cells denoted *S. frugiperda*:pVL-ncFc<sub>c</sub>Rα<sub>591</sub>. Recombinant baculovirus  
20 was plaque purified and amplified from each transfection by methods well known to those skilled in the art, to produce recombinant baculovirus BV-ncFc<sub>c</sub>Rα<sub>591</sub>.

*S. frugiperda*:pVL-ncFc<sub>c</sub>Rα<sub>591</sub> cells were cultured in order to produce a secreted canine Fc<sub>c</sub>R α chain protein, PcFc<sub>c</sub>Rα<sub>4,197</sub> in the following manner. An about 1.5 liter cultures of serum-free ex-Cell Medium was seeded with about 1 x 10<sup>6</sup> *Trichoplusia ni*  
25 cells (High Five™ cells) per ml of medium. The cell culture was inoculated with recombinant baculovirus BV-ncFc<sub>c</sub>Rα<sub>591</sub> at a multiplicity of infection (MOI) of about 2 to about 5 plaque forming units (pfu) per cell to produce recombinant cell *Trichoplusia ni*:BV-ncFc<sub>c</sub>Rα<sub>591</sub>. The infection was allowed to proceed at a controlled temperature of 27°C for 48 hours, to produce recombinant protein of PcFc<sub>c</sub>Rα<sub>4,197</sub>. Following infection,  
30 cells were separated from the medium by centrifugation, and the medium was frozen at -70°C.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT:  
5 (A) NAME: Heska Corporation  
(B) STREET: 1825 Sharp Point Drive  
(C) CITY: Fort Collins  
(D) STATE: CO  
(E) COUNTRY: US  
10 (F) POSTAL CODE (ZIP): 80525  
(G) TELEPHONE: (970) 493-7272  
(H) TELEFAX: (970) 484-9505
- (ii) TITLE OF INVENTION: METHOD TO DETECT CANINE IgE
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
(B) STREET: 28 STATE STREET  
(C) CITY: BOSTON  
(D) STATE: MA  
20 (E) COUNTRY: US  
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: Windows 95  
(D) SOFTWARE: ASCII DOS TEXT
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/833,488  
(B) FILING DATE: 07-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
35 (A) NAME: Rothenberger, Scott D.  
(B) REGISTRATION NUMBER: 41,277  
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 742-4214

## 40 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 30 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCGGATCCA ATATGCCTGC TTCCATGGGA

30

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## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTGGAATTCT TACTCTTTT TCACAATAAT GTTG

34

## 10 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 10..603

(ix) FEATURES:

- (A) NAME/KEY: R = A or G  
 (B) LOCATION: 187

(ix) FEATURES:

- (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCAAT ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG  
 Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu  
 1 5 10

42

TGG CTA GCG CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA  
 Trp Leu Ala Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser  
 15 20 25

84

GAT ACC TTG AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT  
 Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn  
 30 35

126

ACA ATA TTG AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG  
 Thr Ile Leu Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly  
 40 45 50

168

TTC AAC TCC CTT GAA GTC GRC TCT GCT GTG TGG CTC CAC AAC  
 Asn Asn Ser Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn  
 55 60 65

210

AAC ACT ACT TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC AAT  
 Asn Thr Thr Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn  
 70 75 80

252



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	AAA	GCC	CAA	ATC	CAG	GAC	AGT	GGG	GAG	TAC	AGG	TGT	CGG	GAA	294
	Lys	Ala	Gln	Ile	Gln	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Arg	Glu	
			85						90					95	
5	AAT	AGA	TCC	ATC	CTG	AGT	GAT	CCT	GTG	TAC	CTA	ACA	GTC	TTC	336
	Asn	Arg	Ser	Ile	Leu	Ser	Asp	Pro	Val	Tyr	Leu	Thr	Val	Phe	
				100					105						
	ACA	GAG	TGG	CTG	ATC	CTT	CAA	GCC	TCT	GCC	AAC	GTG	GTG	ATG	378
	Thr	Glu	Trp	Leu	Ile	Leu	Gln	Ala	Ser	Ala	Asn	Val	Val	Met	
	110				115						120				
10	GAG	GGT	GAG	AGC	TTC	CTC	ATC	AGG	TGC	CAT	AGT	TGG	AAG	AAT	420
	Glu	Gly	Glu	Ser	Phe	Leu	Ile	Arg	Cys	His	Ser	Trp	Lys	Asn	
	125					130						135			
15	TTG	AGG	CTC	ACA	AAG	GTG	ACC	TAC	TAC	AAG	GAT	GGC	ATC	CCC	462
	Leu	Arg	Leu	Thr	Lys	Val	Thr	Tyr	Tyr	Lys	Asp	Gly	Ile	Pro	
			140					145					150		
	ATC	AGG	TAC	TGG	TAC	GAG	AAC	TTC	AAC	ATC	TCC	ATT	AGC	AAC	504
	Ile	Arg	Tyr	Trp	Tyr	Glu	Asn	Phe	Asn	Ile	Ser	Ile	Ser	Asn	
			155					160						165	
20	GTC	ACA	ACC	AAA	AAC	AGC	GGC	AAC	TAT	TCC	TGC	TCA	GGC	CAG	546
	Val	Thr	Thr	Lys	Asn	Ser	Gly	Asn	Tyr	Ser	Cys	Ser	Gly	Gln	
				170					175						
	ATC	CAG	CAG	AAA	GGC	TAC	ACC	TCT	AAA	GTC	CTC	AAC	ATT	ATT	588
	Ile	Gln	Gln	Lys	Gly	Tyr	Thr	Ser	Lys	Val	Leu	Asn	Ile	Ile	
	180				185						190				
25	GTG	AAA	AAA	GAG	TAA	GAATTC									609
	Val	Lys	Lys	Glu											
			195												

## (2) INFORMATION FOR SEQ ID NO:4:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 amino acids  
 (B) TYPE: nucleic acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 35 (ix) FEATURES:  
 (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala  
 1 5 10

40 Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu  
 15 20 25

Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu  
 30 35 40

45 Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser  
 45 50 55

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Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn Asn Thr Thr  
60 65 70

Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln  
75 80

5 Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser  
85 90 95

Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp  
100 105 110

10 Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu  
115 120 125

Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu  
130 135 140

Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr  
145 150

15 Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr  
155 160 165

Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
170 175 180

20 Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys  
185 190 195  
Glu

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 609 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
30 (A) NAME/KEY: Y = G or T  
(B) LOCATION: 422

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTTAC	TCTTTTTTCA	CAATAATGTT	GAGGACTTTA	GAGGTGTAGC	50
CTTTCTGCTG	GATCTGGCCT	GAGCAGGAAT	AGTTGCCGCT	GTTTTTGGTT	100
GTGACGTTGC	TAATGGAGAT	GTTGAAGTTC	TCGTACCAGT	ACCTGATGGG	150
GATGCCATCC	TTGTAGTAGG	TCACCTTTGT	GAGCCTCAAA	TTCTTCCAAC	200
TATGGCACCT	GATGAGGAAG	CTCTACCCT	CCATCACCAC	GTTGGCAGAG	250
GCTTGAAGGA	TCAGCCACTC	TGTGAAGACT	GTTAGGTACA	CAGGATCACT	300
CAGGATGGAT	CTATTTTCCC	GACACCTGTA	CTCCCCACTG	TCTTGGATT	350
40 GGGCTTTATT	GATGTCCAAA	CGTGAAGTCG	TCTCTTGCA	AGTAGTGTG	400
TTGTGGAGCC	ACACAGCAGA	GYCGACTTCA	AGGGAGTTGT	TCCCAGTACA	450
TGTAAGAGTC	ACACTGTCAT	CCTTCAATAT	TGTATTCCAT	GGCGGGTTCA	500
TGGACACTGT	AGGTTTCAAG	GTATCTGATG	ACATGACACC	TGGAGAGGAG	550
AGCAGCAGCG	CTAGCCACAG	CAGGGCAGGG	CCTCCCATGG	AAGCAGGCAT	600
45 ATTGGATCC					609

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## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..591

(ix) FEATURES:  
 (A) NAME/KEY: R = A or G  
 (B) LOCATION: 179

(ix) FEATURES:  
 (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20	ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG TGG CTA GCG Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala 1 5 10	42
	CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA GAT ACC TTG Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu 15 20 25	84
25	AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu 30 35 40	126
	AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser 45 50 55	168
30	CTT GAA GTC GRC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn Asn Thr Thr 60 65 70	210
35	TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC AAT AAA GCC CAA Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln 75 80	252
	ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser 85 90 95	294
40	ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC TTC ACA GAG TGG Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp 100 105 110	336
	CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG ATG GAG GGT GAG Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu 115 120 125	378
45	AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG AAT TTG AGG CTC Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu 130 135 140	420

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ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC CCC ATC AGG TAC 462  
 Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr  
 145 150

5 TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC AAC GTC ACA ACC 504  
 Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr  
 155 160 165

AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC CAG ATC CAG CAG 546  
 Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
 170 175 180

10 AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT ATT GTG AAA AAA 588  
 Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys  
 185 190 195

GAG 591  
 Glu

## 15 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
 (A) NAME/KEY: Y = C or T  
 (B) LOCATION: 413

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTTTTTC ACAATAATGT TGAGGACTTT AGAGGTGTAG CCTTTCTGCT 50  
 GGATCTGGCC TGAGCAGGAA TAGTTGCCGC TGTTTTGGT TGTGACGTTG 100  
 CTAATGGAGA TGTGAAGTT CTCGTACCAG TACCTGATGG GGATGCCATC 150  
 CTTGTAGTAG GTCACCTTTG TGAGCCTCAA ATTCTTCCAA CTATGGCACC 200  
 30 TGATGAGGAA GCTCTCACCC TCCATCACCA CGTTGGCAGA GGCTTGAAGG 250  
 ATCAGCCACT CTGTGAAGAC TGTAGGTAC ACAGGATCAC TCAGGATGGA 300  
 TCTATTTTCC CGACACCTGT ACTCCCCACT GTCCTGGATT TGGGCTTTAT 350  
 TGATGTCCAA ACGTGAAGTC GTCTCTTGCA AAGTAGTGTT GTTGTGGAGC 400  
 CACACAGCAG AGYCGACTTC AAGGGAGTTG TTCCCAGTAC ATGTAAGAGT 450  
 35 CACACTGTCA TCCTTCAATA TTGTATTCCA TGGCGGGTTC ATGGACACTG 500  
 TAGGTTTCAA GGTATCTGAT GACATGACAC CTGGAGAGGA GAGCAGCAGC 550  
 GCTAGCCACA GCAGGGCAGG GCCTCCCATG GAAGCAGGCA T 591

## (2) INFORMATION FOR SEQ ID NO:8:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 10..604

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- (ix) FEATURES:  
 (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60, 195, 196
- 5 (ix) FEATURES:  
 (A) NAME/KEY: K = G or T  
 (B) LOCATION: 187
- (ix) FEATURES:  
 (A) NAME/KEY: N = unknown nucleotide  
 (B) LOCATION: 592, 595, 596
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- |    |   |     |
|----|---|-----|
|    | GGATCCAAT ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG   | 42  |
|    | Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu             |     |
|    | 1 5 10  |     |
| 15 | TGG CTA GCG CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA | 84  |
|    | Trp Leu Ala Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser |     |
|    | 15 20 25  |     |
|    | GAT ACC TTG AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT | 126 |
|    | Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn |     |
|    | 30 35   |     |
| 20 | ACA ATA TTG AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG | 168 |
|    | Thr Ile Leu Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly |     |
|    | 40 45 50  |     |
| 25 | AAC AAC TCC CTT GAA GTC GKC TCT GCT GTG TGG CTC CAC AAC | 210 |
|    | Asn Asn Ser Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn |     |
|    | 55 60 65  |     |
|    | AAC ACT ACT TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC AAT | 252 |
|    | Asn Thr Thr Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn |     |
|    | 70 75 80  |     |
| 30 | AAA GCC CAA ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA | 294 |
|    | Lys Ala Gln Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu |     |
|    | 85 90 95  |     |
|    | AAT AGA TCC ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC TTC | 336 |
|    | Asn Arg Ser Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe |     |
|    | 100 105   |     |
| 35 | ACA GAG TGG CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG ATG | 378 |
|    | Thr Glu Trp Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met |     |
|    | 110 115 120   |     |
| 40 | GAG GGT GAG AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG AAT | 420 |
|    | Glu Gly Glu Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn |     |
|    | 125 130 135   |     |
|    | TTG AGG CTC ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC CCC | 452 |
|    | Leu Arg Leu Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro |     |
|    | 140 145 150   |     |
| 45 | ATC AGG TAC TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC AAC | 504 |
|    | Ile Arg Tyr Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn |     |
|    | 155 160 165   |     |

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GTC ACA ACC AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC CAG 546  
 Val Thr Thr Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln  
 170 175

5 ATC CAG CAG AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT ATT 588  
 Ile Gln Gln Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile  
 180 185 190

GTG NAA NNA GAG TAA GAATC 609  
 Val Xaa Xaa Glu  
 195

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 amino acids  
 (B) TYPE: amino acids  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(ix) FEATURES:  
 (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60, 195, 196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala  
 1 5 10

Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu  
 15 20 25

25 Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu  
 30 35 40

Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser  
 45 50 55

Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn Asn Thr Thr  
 60 65 70

30 Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln  
 75 80

Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser  
 85 90 95

35 Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp  
 100 105 110

Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu  
 115 120 125

Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu  
 130 135 140

40 Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr  
 145 150

Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr  
 155 160 165

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Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
 170 175 180

Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Xaa Xaa  
 185 190 195

5 Glu

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURES:  
 (A) NAME/KEY: N = any nucleotide  
 (B) LOCATION: 14, 15, 18
- (ix) FEATURES:  
 (A) NAME/KEY: M = A or C  
 (B) LOCATION: 422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20	GAATTCTTAC	TCTNNTTNCA	CAATAATGTT	GAGGACTTTA	GAGGTGTAGC	50
	CTTTCTGCTG	GATCTGGCCT	GAGCAGGAAT	AGTTGCCGCT	GTTTTTGGTT	100
	GTGACGTTGC	TAATGGAGAT	GTTGAAGTTC	TCGTACCACT	ACCTGATGGG	150
	GATGCCATCC	TTGTAGTAGG	TCACCTTTGT	GAGCCTCAAA	TTCTTCCAAC	200
	TATGGCACCT	GATGAGGAAG	CTCTCACCCCT	CCATCACCAC	GTTGGCAGAG	250
25	GCTTGAAGGA	TCAGCCACTC	TGTGAAGACT	GTTAGGTACA	CAGGATCACT	300
	CAGGATGGAT	CTATTTTCCC	GACACCTGTA	CTCCCCACTG	TCCTGGATTT	350
	GGGCTTTATT	GATGTCCAAA	CGTGAAGTCG	TCTCTTGCAA	AGTAGTGTG	400
	TTGTGGAGCC	ACACAGCAGA	GMCGACTTCA	AGGGAGTTGT	TCCAGTACA	450
	TGTAAGAGTC	ACACTGTCAT	CCTTCAATAT	TGTATTCCAT	GGCGGGTTCA	500
30	TGGACACTGT	AGGTTTCAAG	GTATCTGATG	ACATGACACC	TGGAGAGGAG	550
	AGCAGCAGCG	CTAGCCACAG	CAGGGCAGGG	CCTCCCATGG	AAGCAGGCAT	600
	ATTGGATCC					609

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURES:  
 (A) NAME/KEY: Xaa = unknown amino acid  
 (B) LOCATION: 60, 195, 196
- (ix) FEATURES:  
 (A) NAME/KEY: K = G or T  
 (B) LOCATION: 179
- (ix) FEATURES:  
 (A) NAME/KEY: N = unknown nucleotide  
 (B) LOCATION: 583, 586, 587

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## (ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 1..591

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5	ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG TGC CTA GCG	42
	Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala	
	1 5 10	
	CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA GAT ACC TTG	84
10	Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu	
	15 20 25	
	AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG	126
	Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu	
	30 35 40	
15	AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC	168
	Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser	
	45 50 55	
	CTT GAA GTC GKC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT	210
	Leu Glu Val Xaa Ser Ala Val Trp Leu His Asn Asn Thr Thr	
	60 65 70	
20	TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC AAT AAA GCC CAA	252
	Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln	
	75 80	
	ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC	294
25	Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser	
	85 90 95	
	ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC TTC ACA GAG TGG	336
	Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp	
	100 105 110	
30	CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG ATG GAG GGT GAG	378
	Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu	
	115 120 125	
	AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG AAT TTG AGG CTC	420
	Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu	
	130 135 140	
35	ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC CCC ATC AGG TAC	462
	Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr	
	145 150	
	TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC AAC GTC ACA ACC	504
40	Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr	
	155 160 165	
	AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC CAG ATC CAG CAG	546
	Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln	
	170 175 180	
45	AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT ATT GTG NAA NNA	588
	Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Xaa Xaa	
	185 190 195	
	GAG	591
	Glu	



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## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURES:  
 (A) NAME/KEY: N = any nucleotide  
 (B) LOCATION: 5, 6, 9
- (ix) FEATURES:  
 (A) NAME/KEY: M = A or C  
 (B) LOCATION: 413
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

15 CTCTNNTTNC ACAATAATGT TGAGGACTTT AGAGGTGTAG CCTTTCTGCT      50
   GGATCTGGCC TGAGCAGGAA TAGTTGCCGC TGTTTTTGGT TGTGACGTTG      100
   CTAATGGAGA TGTGAAGTT CTCGTACCAG TACCTGATGG GGATGCCATC      150
   CTTGTAGTAG GTCACCTTTG TGAGCCTCAA ATTCTTCCAA CTATGGCACC      200
   TGATGAGGAA GCTCTCACCC TCCATCACCA CGTTGGCAGA GGCTTGAAGG      250
20 ATCAGCCACT CTGTGAAGAC TGTTAGGTAC ACAGGATCAC TCAGGATGGA      300
   TCTATTTTCC CGACACCTGT ACTCCCCACT GTCCTGGATT TGGGCTTTAT      350
   TGATGTCCAA ACGTGAAGTC GTCTCTTGCA AAGTAGTGTT GTTGTGGAGC      400
   CACACAGCAG AGMCGACTTC AAGGGAGTTG TTCCCAGTAC ATGTAAGAGT      450
   CACACTGTCA TCCTTCAATA TTGTATTCCA TGGCGGGTTC ATGGACACTG      500
25 TAGGTTTCAA GGTATCTGAT GACATGACAC CTGGAGAGGA GAGCAGCAG      550
   GCTAGCCACA GCAGGGCAGG GCCTCCCATG GAAGCAGGCA T              591

```

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 617 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 10..606
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

40 GGATCCAAT ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG      42
   Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu
   1              5              10

   TGG CTA GCG CTG CTG CTC TCC TCT CCA GGT GTC GTG TCA TCA      84
   Trp Leu Ala Leu Leu Leu Ser Ser Pro Gly Val Val Ser Ser
   15              20              25

45 GAT ACC TTG AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT      126
   Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn
   30              35

   ACA ATA TTG AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG      168
   Thr Ile Leu Lys Asp Ser Val Thr Leu Thr Cys Thr Gly
   40              45              50

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:14:

```

35      (i)      SEQUENCE CHARACTERISTICS:
              (A)  LENGTH:  199 amino acids
              (B)  TYPE:    amino acid
              (D)  TOPOLOGY: linear

              (ii)     MOLECULE TYPE:  protein

40      (xi)     SEQUENCE DESCRIPTION:  SEQ ID NO:14:

Met  Pro  Ala  Ser  Met  Gly  Gly  Pro  Ala  Leu  Leu  Trp  Leu  Ala
 1              5              10
Leu  Leu  Leu  Ser  Ser  Pro  Gly  Val  Val  Ser  Ser  Asp  Thr  Leu
15              20              25
45  Lys  Pro  Thr  Val  Ser  Met  Asn  Pro  Pro  Trp  Asn  Thr  Ile  Leu
      30              35              40

```

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[illegible]

(2) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 617 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	GAATTCCTAG	AATTCTTACT	CTTTTTCACA	ATAATGTTGA	GGACTTTAGA	50
	GGTGTAGCCT	TTCTGCTGGA	TCTGGCCTGA	GCAGGAATAG	TTGCCGCTGT	100
35	TTTGGTGTG	GACGTTGCCTA	ATGGAGATGT	TGAAGTTCTC	GTACCAGTAC	150
	CTGATGGGGA	TGCCATCCCTT	GTAGTAGGTC	ACCTTTGTGA	GCCTCAAAAT	200
	CTTCCAACCTA	TGGCACCTGA	TGAGGAAGCT	CTCACCTCC	ATCACCACGT	250
	TGGCAGAGGC	TTGAAGGATC	AGCCACTCTG	TGAAGACTGT	TAGGTACACA	300
	GGATCACTCA	GGATGGATCT	ATTTTCCCGA	CACCTGTACT	CCCCACTGTC	350
40	CTGGATTTGG	GCTTTATTGA	TGTTCAAACG	TGAAGTCGTC	TCTTGCAAAG	400
	TAGTGTGTGT	GTGGAGCCAC	ACACGAGAGT	CGAATTC AAG	GGAGTTGTTC	450
	CCAGTACATG	TAAGAGTCAC	ACTGTCATCC	TTCAATATTG	TATTCCATGG	500
	CGGGTTCATG	GACACTGTAG	GTTTCAAGGT	ATCTGATGAC	ACGACACCTG	550
	GAGAGGAGAG	CAGCAGCGCT	AGCCACAGCA	GGGCAGGGCC	TCCCATGGAA	600
	GCAGGCATAT	TGGATCC				617

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## (2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 597 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG TGG CTA GCG	42
	Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala	
	1 5 10	
15	CTG CTG CTC TCC TCT CCA GGT GTC GTG TCA TCA GAT ACC TTG	84
	Leu Leu Leu Ser Ser Pro Gly Val Val Ser Ser Asp Thr Leu	
	15 20 25	
20	AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG	126
	Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu	
	30 35 40	
	AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC	168
	Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser	
	45 50 55	
25	CTT GAA GTC GAC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT	210
	Leu Glu Val Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr	
	60 65 70	
	TTG CAA GAG ACG ACT TCA CGT TTG AAC ATC AAT AAA GCC CAA	252
	Leu Gln Glu Thr Thr Ser Arg Leu Asn Ile Asn Lys Ala Gln	
	75 80	
30	ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC	294
	Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser	
	85 90 95	
35	ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC TTC ACA GAG TGG	336
	Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp	
	100 105 110	
	CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG ATG GAG GGT GAG	378
	Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu	
	115 120 125	
40	AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG AAT TTG AGG CTC	420
	Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu	
	130 135 140	
	ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC CCC ATC AGG TAC	462
	Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr	
	145 150	
45	TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC AAC GTC ACA ACC	504
	Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr	
	155 160 165	

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AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC CAG ATC CAG CAG 546  
 Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
 170 175 180

5 AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT ATT GTG AAA AAG 588  
 Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys  
 185 190 195

AGT AAG AAT 597  
 Ser Lys Asn

(2) INFORMATION FOR SEQ ID NO:17:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 597 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATTCTTACTC TTTTTCACAA TAATGTTGAG GACTTTAGAG GTGTAGCCTT 50  
 TCTGCTGGAT CTGGCCTGAG CAGGAATAGT TGCCGCTGTT TTTGGTTGTG 100  
 20 ACGTTGCTAA TGGAGATGTT GAAGTTCTCG TACCAGTACC TGATGGGGAT 150  
 GCCATCCTTG TAGTAGGTCA CCTTTGTGAG CCTCAAATTC TTCCAACATAT 200  
 GGCACCTGAT GAGGAAGCTC TCACCCTCCA TCACCACGTT GGCAGAGGCT 250  
 TGAAGGATCA GCCACTCTGT GAAGACTGTT AGGTACACAG GATCACTCAG 300  
 GATGGATCTA TTTTCCCGAC ACCTGTACTC CCCACTGTCC TGGATTTGGG 350  
 25 CTTTATTGAT GTTCAAACGT GAAGTCGTCT CTTGCAAAGT AGTGTTGTTG 400  
 TGGAGCCACA CAGCAGAGTC GACTTCAAGG GAGTTGTTCC CAGTACATGT 450  
 AAGAGTCACA CTGTATCCT TCAATATTGT ATTCCATGGC GGGTTCATGG 500  
 ACACTGTAGG TTTCAAGGTA TCTGATGACA CGACACCTGG AGAGGAGAGC 550  
 AGCAGCGCTA GCCACAGCAG GGCAGGGCCT CCCATGGAAG CAGGCAT 597

(2) INFORMATION FOR SEQ ID NO:18:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- 35 (ix) FEATURES:  
 (A) NAME/KEY: Xaa = any amino acid  
 (B) LOCATION: 9, 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40 Ser Asp Thr Leu Lys Pro Thr Val Xaa Met Asn Pro Pro Xaa  
 1 5 10

Asn Leu Ile  
 15

(2) INFORMATION FOR SEQ ID NO:19:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 991 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 35..796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5	CTCCAGTCCA GTCGTACGTG GGGGCCACGA GGAG ATG CCT GCT	43
	Met Pro Ala	
	1	
10	TCC ATG GGA GGC CCT GCC CTG CTG TGG CTA GCG CTG CTG CTC	85
	Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala Leu Leu	
	5 10 15	
	TCC TCT CCA GGT GTC ATG TCA TCA GAT ACC TTG AAA CCT ACA	127
	Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu Lys Pro Thr	
	20 25 30	
15	GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG AAG GAT GAC	169
	Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu Lys Asp Asp	
	35 40 45	
20	AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC CTT GAA GTC	211
	Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser Leu Glu Val	
	50 55	
	GAC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT TTG CAA GAG	253
	Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr Leu Gln Glu	
	60 65 70	
25	ACG ACT TCA CGT TTG GAC ATC AAT AAA GCC CAA ATC CAG GAC	295
	Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln Ile Gln Asp	
	75 80 85	
	AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC ATC CTG AGT	337
	Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser Ile Leu Ser	
	90 95 100	
30	GAT CCT GTG TAC CTA ACA GTC TTC ACA GAG TGG CTG ATC CTT	379
	Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp Leu Ile Leu	
	105 110 115	
35	CAA GCC TCT GCC AAC GTG GTG ATG GAG GGT GAG AGC TTC CTC	421
	Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu Ser Phe Leu	
	120 125	
	ATC AGG TGC CAT AGT TGG AAG AAT TTG AGG CTC ACA AAG GTG	463
	Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu Thr Lys Val	
	130 135 140	
40	ACC TAC TAC AAG GAT GGC ATC CCC ATC AGG TAC TGG TAC GAG	505
	Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr Trp Tyr Glu	
	145 150 155	
	AAC TTC AAC ATC TCC ATT AGC AAC GTC ACA ACC AAA AAC AGC	437
	Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr Lys Asn Ser	
	160 165 170	
45	GGC AAC TAT TCC TGC TCA GGC CAG ATC CAG CAG AAA GGC TAC	589
	Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln Lys Gly Tyr	
	175 180 185	

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ACC TCT AAA GTC CTC AAC ATT ATT GTG AAA AAA GAG CCC ACC 631  
 Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys Glu Pro Thr  
 190 195

5 AAG CAA AAC AAG TAC TCC GGG CTA CAA TTC CTG ATC CCG TTG 673  
 Lys Gln Asn Lys Tyr Ser Gly Leu Gln Phe Leu Ile Pro Leu  
 200 205 210

GTG GTG GTG ATT CTG TTT GCT GTG GAC ACA GGA CTG TTT ATC 715  
 Val Val Val Ile Leu Phe Ala Val Asp Thr Gly Leu Phe Ile  
 215 220 225

10 TCG ACC AAG CAG CAG TTG ACA GTG CTC TTG CAG ATT AAG AGG 757  
 Ser Thr Lys Gln Gln Leu Thr Val Leu Leu Gln Ile Lys Arg  
 230 235 240

ACC AGG AAG AAC AAA AAG CCA GAA CCC GGA AAG AAC TGA 796  
 Thr Arg Lys Asn Lys Lys Pro Glu Pro Gly Lys Asn  
 15 245 250

TGCCGCTGCT TAAGAAACAT CAGCATCAGC AATCGCTTCT CCATCGTCAG 846  
 ACGCAGCTCA CGATGCACAC GGGAAGGTCT GCAGTCATGG CTTTGCAGAA 896  
 CTGCTTCATT CAACCAACTC AAAGTGATTA AGTGGCATGT GATAGTAGGT 946  
 GCTCAATAAA CCGCAGTTAG ATAAATAAAA AAAAAAAAAA AAAAA 991

## 20 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala  
 1 5 10

30 Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu  
 15 20 25

Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu  
 30 35 40

Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser  
 45 50 55

35 Leu Glu Val Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr  
 60 65 70

Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln  
 75 80

40 Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser  
 85 90 95

Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp  
 100 105 110

Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu  
 115 120 125

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Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu  
130 135 140

Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr  
145 150

5 Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr  
155 160 165

Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
170 175 180

10 Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys  
185 190 195

Glu Pro Thr Lys Gln Asn Lys Tyr Ser Gly Leu Gln Phe Leu  
200 205 210

Ile Pro Leu Val Val Val Ile Leu Phe Ala Val Asp Thr Gly  
215 220

15 Leu Phe Ile Ser Thr Lys Gln Gln Leu Thr Val Leu Leu Gln  
225 230 235

Ile Lys Arg Thr Arg Lys Asn Lys Lys Pro Glu Pro Gly Lys  
240 245 250

Asn

## 20 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 991 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

	TTTTTTTTTT	TTTTTTTTTT	TTTATCTAAC	TGCCGTTTAT	TGAGCACCTA	50
	CTATCACATG	CCACTTAATC	AGTTTGAGTT	GGTTGAATGA	AGCAGTTCTG	100
30	CAAAGCCATG	ACTGCAGACC	TTCCCGTGTG	CATCGTGAGC	TGCGTCTGAC	150
	GATGGAGAAG	CGATTGCTGA	TGCTGATGTT	TCTTAAGCAG	CGGCATCAGT	200
	TCTTTCCGGG	TTCTGGCTTT	TTGTCTCTCC	TGGTCCTCTT	AATCTGCAAG	250
	AGCACTGTCA	ACTGCTGCTT	GGTCGAGATA	AACAGTCCTG	TGTCCACAGC	300
	AAACAGAATC	ACCACCACCA	ACGGGATCAG	GAATTGTAGC	CCGGAGTACT	350
35	TGTTTTGCTT	GGTGGGCTCT	TTTTTCACAA	TAATGTTGAG	GACTTTAGAG	400
	GTGTAGCCTT	TCTGCTGGAT	CTGGCCTGAG	CAGGAATAGT	TGCCGCTGTT	450
	TTTGGTGTG	ACGTTGCTAA	TGGAGATGTT	GAAGTCTCTG	TACCAGTACC	500
	TGATGGGGAT	GCCATCCTTG	TAGTAGGTCA	CCTTTGTGAG	CCTCAAATTC	550
	TTCCAACTAT	GGCACCTGAT	GAGGAAGCTC	TCACCCTCCA	TCACCACGTT	600
40	GGCAGAGGCT	TGAAGGATCA	GCCACTCTGT	GAAGACTGTT	AGGTACACAG	650
	GATCACTCAG	GATGGATCTA	TTTTCCCGA	CTCTGTACTC	CCCACTGTCC	700
	TGGATTTGGG	CTTTATTGAT	GTCCAAACGT	GAAGTCGTCT	CTTGCAAAGT	750
	AGTGTGTGTT	TGGAGCCACA	CAGCAGAGTC	GACTTCAAGG	GAGTGTGTC	800
	CAGTACATGT	AAGAGTCACA	CTGTATCCTT	TCAATATTGT	ATTCCATGGC	850
45	GGGTTTCATG	ACACTGTAGG	TTTCAAGGTA	TCTGATGACA	TGACACCTGG	900
	AGAGGAGAGC	AGCAGCGCTA	GCCACAGCAG	GGCAGGGCCT	CCCATGGAAG	950
	CAGGCATCTC	CTCGTGGCCC	CCACGTACGA	CTGGACTGGA	G	991



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## (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 759 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG TGG CTA GCG	42
	Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala	
	1 5 10	
15	CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA GAT ACC TTG	84
	Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu	
	15 20 25	
20	AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG	126
	Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu	
	30 35 40	
	AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC	168
	Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser	
	45 50 55	
25	CTT GAA GTC GAC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT	210
	Leu Glu Val Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr	
	60 65 70	
	TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC AAT AAA GCC CAA	252
	Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln	
	75 80	
30	ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC	294
	Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser	
	85 90 95	
35	ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC TTC ACA GAG TGG	336
	Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp	
	100 105 110	
	CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG ATG GAG GGT GAG	378
	Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu	
	115 120 125	
40	AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG AAT TTG AGG CTC	420
	Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu	
	130 135 140	
	ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC CCC ATC AGG TAC	462
	Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr	
	145 150	
45	TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC AAC GTC ACA ACC	504
	Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr	
	155 160 165	

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	AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC CAG ATC CAG CAG	546
	Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln	
	170 175 180	
5	AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT ATT GTG AAA AAA	588
	Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys	
	185 190 195	
	GAG CCC ACC AAG CAA AAC AAG TAC TCC GGG CTA CAA TTC CTG	630
	Glu Pro Thr Lys Gln Asn Lys Tyr Ser Gly Leu Gln Phe Leu	
	200 205 210	
10	ATC CCG TTG GTG GTG GTG ATT CTG TTT GCT GTG GAC ACA GGA	672
	Ile Pro Leu Val Val Val Ile Leu Phe Ala Val Asp Thr Gly	
	215 220	
	CTG TTT ATC TCG ACC AAG CAG CAG TTG ACA GTG CTC TTG CAG	714
	Leu Phe Ile Ser Thr Lys Gln Gln Leu Thr Val Leu Leu Gln	
15	225 230 235	
	ATT AAG AGG ACC AGG AAG AAC AAA AAG CCA GAA CCC GGA AAG	756
	Ile Lys Arg Thr Arg Lys Asn Lys Lys Pro Glu Pro Gly Lys	
	240 245 250	
20	AAC	759
	Asn	

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 759 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	GTTCTTTCCG GGTTCTGGCT TTTTGTTCTT CCTGGTCCTC TTAATCTGCA	50
30	AGAGCACTGT CAACTGCTGC TTGGTCGAGA TAAACAGTCC TGTGTCCACA	100
	GCAAACAGAA TCACCACCAC CAACGGGATC AGGAATTGTA GCCCGGAGTA	150
	CTTGTTTTGC TTGGTGGGCT CTTTTTTCAC AATAATGTTG AGGACTTTAG	200
	AGGTGTAGCC TTTCTGCTGG ATCTGGCCTG AGCAGGAATA GTTGCCGCTG	250
	TTTTTTGGTTG TGACGTTGCT AATGGAGATG TTGAAGTTCT CGTACCAGTA	300
35	CCTGATGGGG ATGCCATCCT TGTAGTAGGT CACCTTTGTG AGCCTCAAAT	350
	TCTTCCAACT ATGGCACCTG ATGAGGAAGC TCTCACCCTC CATCACCACG	400
	TTGGCAGAGG CTTGAAGGAT CAGCCACTCT GTGAAGACTG TTAGGTACAC	450
	AGGATCACTC AGGATGGATC TATTTTCCCG ACACCTGTAC TCCCCACTGT	500
	CCTGGATTGG GGCTTTATTG ATGTCCAAAC GTGAAGTCGT CTCTTGCAA	550
40	GTAGTGTGTG TGTGGAGCCA CACAGCAGAG TCGACTTCAA GGGAGTTGTT	600
	CCCAGTACAT GTAAGAGTCA CACTGTCATC CTTCAATATT GTATTCCATG	650
	GCGGGTTCAT GGACACTGTA GGTTC AAGG TATCTGATGA CATGACACCT	700
	GGAGAGGAGA GCAGCAGCGC TAGCCACAGC AGGGCAGGGC CTCCCATGGA	750
	AGCAGGCAT	759

## 45 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp  
 1 5 10  
 5 Asn Thr Ile Leu Lys Asp Asp Ser Val Thr Leu Thr Cys Thr  
 15 20 25  
 Gly Asn Asn Ser Leu Glu Val Asp Ser Ala Val Trp Leu His  
 30 35 40  
 Asn Asn Thr Thr Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile  
 45 50 55  
 10 Asn Lys Ala Gln Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg  
 60 65 70  
 Glu Asn Arg Ser Ile Leu Ser Asp Pro Val Tyr Leu Thr Val  
 75 80  
 15 Phe Thr Glu Trp Leu Ile Leu Gln Ala Ser Ala Asn Val Val  
 85 90 95  
 Met Glu Gly Glu Ser Phe Leu Ile Arg Cys His Ser Trp Lys  
 100 105 110  
 Asn Leu Arg Leu Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile  
 115 120 125  
 20 Pro Ile Arg Tyr Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser  
 130 135 140  
 Asn Val Thr Thr Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly  
 145 150  
 25 Gln Ile Gln Gln Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile  
 155 160 165  
 Ile Val Lys Lys Glu Pro Thr Lys Gln Asn Lys Tyr Ser Gly  
 170 175 180  
 Leu Gln Phe Leu Ile Pro Leu Val Val Val Ile Leu Phe Ala  
 185 190 195  
 30 Val Asp Thr Gly Leu Phe Ile Ser Thr Lys Gln Gln Leu Thr  
 200 205 210  
 Val Leu Leu Gln Ile Lys Arg Thr Arg Lys Asn Lys Lys Pro  
 215 220  
 35 Glu Pro Gly Lys Asn  
 225

## (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCGAAGATCT ATAAATATGC CTGCTTCCAT GGG

33

(2) INFORMATION FOR SEQ ID NO:26:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCAGGAATTC TTACTCTTTT TTCACAATAA TGT

33

(2) INFORMATION FOR SEQ ID NO:27:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25	ATG CCT GCT TCC ATG GGA GGC CCT GCC CTG CTG TGG CTA GCG Met Pro Ala Ser Met Gly Gly Pro Ala Leu Leu Trp Leu Ala 1 5 10	42
	CTG CTG CTC TCC TCT CCA GGT GTC ATG TCA TCA GAT ACC TTG Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu 15 20 25	84
30	AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG AAT ACA ATA TTG Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu 30 35 40	126
	AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT GGG AAC AAC TCC Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser 45 50 55	168
35	CTT GAA GTC GAC TCT GCT GTG TGG CTC CAC AAC AAC ACT ACT Leu Glu Val Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr 60 65 70	210
40	TTG CAA GAG ACG ACT TCA CTT TTG GAC ATC AAT AAA GCC CAA Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln 75 80	252
	ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG GAA AAT AGA TCC Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser 85 90 95	294

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	ATC	CTG	AGT	GAT	CCT	GTG	TAC	CTA	ACA	GTC	TTC	ACA	GAG	TGG	336
	Ile	Leu	Ser	Asp	Pro	Val	Tyr	Leu	Thr	Val	Phe	Thr	Glu	Trp	
		100					105					110			
5	CTG	ATC	CTT	CAA	GCC	TCT	GCC	AAC	GTG	GTG	ATG	GAG	GGT	GAG	378
	Leu	Ile	Leu	Gln	Ala	Ser	Ala	Asn	Val	Val	Met	Glu	Gly	Glu	
			115					120					125		
	AGC	TTC	CTC	ATC	AGG	TGC	CAT	AGT	TGG	AAG	AAT	TTG	AGG	CTC	420
	Ser	Phe	Leu	Ile	Arg	Cys	His	Ser	Trp	Lys	Asn	Leu	Arg	Leu	
				130					135					140	
10	ACA	AAG	GTG	ACC	TAC	TAC	AAG	GAT	GGC	ATC	CCC	ATC	AGG	TAC	462
	Thr	Lys	Val	Thr	Tyr	Tyr	Lys	Asp	Gly	Ile	Pro	Ile	Arg	Tyr	
					145				150						
	TGG	TAC	GAG	AAC	TTC	AAC	ATC	TCC	ATT	AGC	AAC	GTC	ACA	ACC	504
15	Trp	Tyr	Glu	Asn	Phe	Asn	Ile	Ser	Ile	Ser	Asn	Val	Thr	Thr	
	155					160					165				
	AAA	AAC	AGC	GGC	AAC	TAT	TCC	TGC	TCA	GGC	CAG	ATC	CAG	CAG	546
	Lys	Asn	Ser	Gly	Asn	Tyr	Ser	Cys	Ser	Gly	Gln	Ile	Gln	Gln	
		170					175					180			
20	AAA	GGC	TAC	ACC	TCT	AAA	GTC	CTC	AAC	ATT	ATT	GTG	AAA	AAA	588
	Lys	Gly	Tyr	Thr	Ser	Lys	Val	Leu	Asn	Ile	Ile	Val	Lys	Lys	
			185					190					195		
	GAG														591
	Glu														

## (2) INFORMATION FOR SEQ ID NO:28:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 196 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
- Met Pro Ala Ser Met Gly Gly Pro Ala Leu Trp Leu Ala  
 1 5 10
- Leu Leu Leu Ser Ser Pro Gly Val Met Ser Ser Asp Thr Leu  
 15 20 25
- 35 Lys Pro Thr Val Ser Met Asn Pro Pro Trp Asn Thr Ile Leu  
 30 35 40
- Lys Asp Asp Ser Val Thr Leu Thr Cys Thr Gly Asn Asn Ser  
 45 50 55
- 40 Leu Glu Val Asp Ser Ala Val Trp Leu His Asn Asn Thr Thr  
 60 65
- Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile Asn Lys Ala Gln  
 70 75 80
- Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg Glu Asn Arg Ser  
 85 90 95

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Ile Leu Ser Asp Pro Val Tyr Leu Thr Val Phe Thr Glu Trp  
 100 105 110

Leu Ile Leu Gln Ala Ser Ala Asn Val Val Met Glu Gly Glu  
 115 120 125

5 Ser Phe Leu Ile Arg Cys His Ser Trp Lys Asn Leu Arg Leu  
 130 135

Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile Pro Ile Arg Tyr  
 140 145 150

10 Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser Asn Val Thr Thr  
 155 160 165

Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly Gln Ile Gln Gln  
 170 175 180

Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile Ile Val Lys Lys  
 185 190 195

15 Glu

## (2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25	CTCTTTTTTC	ACAATAATGT	TGAGGACTTT	AGAGGTGTAG	CCTTTCTGCT	50
	GGATCTGGCC	TGAGCAGGAA	TAGTTGCCGC	TGTTTTGGT	TGTGACGTTG	100
	CTAATGGAGA	TGTTGAAGTT	CTCGTACCAG	TACCTGATGG	GGATGCCATC	150
	CTTGTAAGTAG	GTCACCTTTG	TGAGCCTCAA	ATTCTTCCAA	CTATGGCACC	200
	TGATGAGGAA	GCTCTCACCC	TCCATCACCA	CGTTGGCAGA	GGCTTGAAGG	250
	ATCAGCCACT	CTGTGAAGAC	TGTTAGGTAC	ACAGGATCAC	TCAGGATGGA	300
30	TCTATTTTCC	CGACACCTGT	ACTCCCCACT	GTCCTGGATT	TGGGCTTTAT	350
	TGATGTCCAA	ACGTGAAGTC	GTCTCTTGCA	AAGTAGTGTT	GTTGTGGAGC	400
	CACACAGCAG	AGTCGACTTC	AAGGGAGTTG	TTCCCAGTAC	ATGTAAGAGT	450
	CACACTGTCA	TCCTTCAATA	TTGTATTCCA	TGGCGGGTTC	ATGGACACTG	500
	TAGGTTTCAA	GGTATCTGAT	GACATGACAC	CTGGAGAGGA	GAGCAGCAGC	550
35	GCTAGCCACA	GCAGGGCAGG	GCCTCCCATG	GAAGCAGGCA	T	591

## (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 687 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..687

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

	TCA GAT ACC TTG AAA CCT ACA GTG TCC ATG AAC CCG CCA TGG	42
	Ser Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp	
	1 5 10	
5	AAT ACA ATA TTG AAG GAT GAC AGT GTG ACT CTT ACA TGT ACT	84
	Asn Thr Ile Leu Lys Asp Asp Ser Val Thr Leu Thr Cys Thr	
	15 20 25	
10	GGG AAC AAC TCC CTT GAA GTC GAC TCT GCT GTG TGG CTC CAC	126
	Gly Asn Asn Ser Leu Glu Val Asp Ser Ala Val Trp Leu His	
	30 35 40	
	AAC AAC ACT ACT TTG CAA GAG ACG ACT TCA CGT TTG GAC ATC	168
	Asn Asn Thr Thr Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile	
	45 50 55	
15	AAT AAA GCC CAA ATC CAG GAC AGT GGG GAG TAC AGG TGT CGG	210
	Asn Lys Ala Gln Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg	
	60 65 70	
	GAA AAT AGA TCC ATC CTG AGT GAT CCT GTG TAC CTA ACA GTC	252
	Glu Asn Arg Ser Ile Leu Ser Asp Pro Val Tyr Leu Thr Val	
	75 80	
20	TTC ACA GAG TGG CTG ATC CTT CAA GCC TCT GCC AAC GTG GTG	294
	Phe Thr Glu Trp Leu Ile Leu Gln Ala Ser Ala Asn Val Val	
	85 90 95	
25	ATG GAG GGT GAG AGC TTC CTC ATC AGG TGC CAT AGT TGG AAG	336
	Met Glu Gly Glu Ser Phe Leu Ile Arg Cys His Ser Trp Lys	
	100 105 110	
	AAT TTG AGG CTC ACA AAG GTG ACC TAC TAC AAG GAT GGC ATC	378
	Asn Leu Arg Leu Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile	
	115 120 125	
30	CCC ATC AGG TAC TGG TAC GAG AAC TTC AAC ATC TCC ATT AGC	420
	Pro Ile Arg Tyr Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser	
	130 135 140	
	AAC GTC ACA ACC AAA AAC AGC GGC AAC TAT TCC TGC TCA GGC	462
	Asn Val Thr Thr Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly	
	145 150	
35	CAG ATC CAG CAG AAA GGC TAC ACC TCT AAA GTC CTC AAC ATT	504
	Gln Ile Gln Gln Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile	
	155 160 165	
40	ATT GTG AAA AAA GAG CCC ACC AAG CAA AAC AAG TAC TCC GGG	546
	Ile Val Lys Lys Glu Pro Thr Lys Gln Asn Lys Tyr Ser Gly	
	170 175 180	
	CTA CAA TTC CTG ATC CCG TTG GTG GTG GTG TTT GCT	588
	Leu Gln Phe Leu Ile Pro Leu Val Val Ile Leu Phe Ala	
	185 190 195	
45	GTG GAC ACA GGA CTG TTT ATC TCG ACC AAG CAG CAG TTG ACA	630
	Val Asp Thr Gly Leu Phe Ile Ser Thr Lys Gln Gln Leu Thr	
	200 205 210	

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GTG CTC TTG CAG ATT AAG AGG ACC AGG AAG AAC AAA AAG CCA 672  
 Val Leu Leu Gln Ile Lys Arg Thr Arg Lys Asn Lys Lys Pro  
                   215                                  220

5 GAA CCC GGA AAG AAC 687  
 Glu Pro Gly Lys Asn  
 225

## (2) INFORMATION FOR SEQ ID NO:31:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 173 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 Ser Asp Thr Leu Lys Pro Thr Val Ser Met Asn Pro Pro Trp  
     1                                  5                                  10  
 Asn Thr Ile Leu Lys Asp Asp Ser Val Thr Leu Thr Cys Thr  
     15                                  20                                  25  
 Gly Asn Asn Ser Leu Glu Val Asp Ser Ala Val Trp Leu His  
     30                                  35                                  40  
 20 Asn Asn Thr Thr Leu Gln Glu Thr Thr Ser Arg Leu Asp Ile  
                   45                                  50                                  55  
 Asn Lys Ala Gln Ile Gln Asp Ser Gly Glu Tyr Arg Cys Arg  
                   60                                  65                                  70  
 25 Glu Asn Arg Ser Ile Leu Ser Asp Pro Val Tyr Leu Thr Val  
                                   75                                  80  
 Phe Thr Glu Trp Leu Ile Leu Gln Ala Ser Ala Asn Val Val  
     85                                  90                                  95  
 Met Glu Gly Glu Ser Phe Leu Ile Arg Cys His Ser Trp Lys  
     100                                  105                                  110  
 30 Asn Leu Arg Leu Thr Lys Val Thr Tyr Tyr Lys Asp Gly Ile  
                   115                                  120                                  125  
 Pro Ile Arg Tyr Trp Tyr Glu Asn Phe Asn Ile Ser Ile Ser  
                   130                                  135                                  140  
 35 Asn Val Thr Thr Lys Asn Ser Gly Asn Tyr Ser Cys Ser Gly  
                                   145                                  150  
 Gln Ile Gln Gln Lys Gly Tyr Thr Ser Lys Val Leu Asn Ile  
     155                                  160                                  165  
 Ile Val Lys Lys Glu  
     170



While various embodiments of the present invention have been described in detail, it is apparent that modifications and adaptations of those embodiments will occur to those skilled in the art. It is to be expressly understood, however, that such modifications and adaptations are within the scope of the present invention, as set forth

5 in the following claims.

What is claimed is:

1. A method to detect canine IgE comprising:
  - (a) contacting an isolated canine  $Fc_\epsilon R$  receptor ( $Fc_\epsilon R$ ) molecule with a putative canine IgE-containing composition under conditions suitable for formation of a  $Fc_\epsilon R$  molecule:IgE complex; and
  - (b) determining the presence of IgE by detecting said  $Fc_\epsilon R$  molecule:IgE complex, the presence of said  $Fc_\epsilon R$  molecule:IgE complex indicating the presence of IgE.
2. A kit for detecting IgE comprising a canine  $Fc_\epsilon R$  molecule and a means for detecting canine IgE.
3. A method to detect canine flea allergy dermatitis comprising:
  - (a) immobilizing a flea allergen on a substrate;
  - (b) contacting said flea allergen with a putative canine IgE-containing composition under conditions suitable for formation of an antigen:IgE complex bound to said substrate;
  - (c) removing non-bound material from said substrate under conditions that retain antigen:IgE complex binding to said substrate; and
  - (d) detecting the presence of said antigen:IgE complex by contacting said antigen:IgE complex with a canine  $Fc_\epsilon R$  molecule.
4. A kit for detecting flea allergy dermatitis comprising a canine  $Fc_\epsilon R$  receptor molecule and a flea allergen.
5. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule comprises at least a portion of a  $Fc_\epsilon R$  alpha chain that binds to canine IgE.
6. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule comprises a protein selected from the group consisting of  $PcFc_\epsilon R\alpha 1_{197}$ ,  $PcFc_\epsilon R\alpha 2_{197}$ ,  $PcFc_\epsilon R\alpha 3_{199}$ ,  $PcFc_\epsilon R\alpha 4_{253}$ ,  $PcFc_\epsilon R\alpha 4_{229}$ ,  $PcFc_\epsilon R\alpha 4_{173}$  and  $PcFc_\epsilon R\alpha 4_{197}$ .
7. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule is encoded by a nucleic acid molecule selected from the group consisting of  $ncFc_\epsilon R\alpha 1_{609}$ ,  $ncFc_\epsilon R\alpha 1_{591}$ ,  $ncFc_\epsilon R\alpha 2_{609}$ ,  $ncFc_\epsilon R\alpha 2_{591}$ ,  $ncFc_\epsilon R\alpha 3_{617}$ ,  $ncFc_\epsilon R\alpha 3_{597}$ ,  $ncFc_\epsilon R\alpha 4_{591}$ ,  $ncFc_\epsilon R\alpha 4_{687}$ ,  $ncFc_\epsilon R\alpha 4_{991}$  and  $ncFc_\epsilon R\alpha 4_{759}$ .

8. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule is encoded by a nucleic acid molecule selected from the group consisting of: a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:16, SEQ ID NO:19, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:27 and SEQ ID NO:30, and a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule comprising any of said nucleic acid sequences.

9. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule is conjugated to a detectable marker.

10. The invention of Claims 1, 2, 3 or 4, wherein said  $Fc_\epsilon R$  molecule is conjugated to a detectable marker selected from the group consisting of a radioactive label, a fluorescent label, a chemiluminescent label, a chromophoric label and a ligand.

11. The invention of Claims 1 or 3, wherein said putative canine IgE-containing composition comprises a bodily fluid selected from the group consisting of serum, blood and plasma.

12. The method of Claim 1 further comprising the step selected from the group consisting of: binding said canine  $Fc_\epsilon R$  molecule to a substrate prior to performing step (a) to form a  $Fc_\epsilon R$  molecule-coated substrate; and binding said putative IgE-containing composition to a substrate prior to performing step (a) to form a putative IgE-containing composition-coated substrate, wherein said substrate to be bound to said composition is selected from the group consisting of a non-coated substrate, an antigen-coated substrate and an anti-IgE antibody-coated substrate.

13. The method of Claim 12, wherein said antigen is selected from the group consisting of an allergen and a parasitic antigen.

14. The invention of Claims 13 or 30, wherein said allergen is derived from material selected from the group consisting of fungi, trees, weeds, shrubs, grasses, wheat, corn, soybean, rice, eggs, milk, cheese, bovine, poultry, swine, sheep, yeast, fleas, flies, mosquitos, mites, midges, biting gnats, lice, bees, wasps, ants, true bugs and ticks.

15. The invention of Claims 3 or 4, wherein said flea allergen is a flea saliva antigen.

16. The invention of Claims 3 or 4, wherein said flea allergen is selected from the group consisting of flea saliva products and flea saliva proteins.

17. The method of Claim 12, further comprising removing non-bound material from said antigen-coated substrate or said antibody-coated substrate under  
5 conditions that retain antigen or antibody binding to said substrate.

18. The method of Claim 12 or 33, wherein said substrate comprises an ELISA plate, a dipstick, a radioimmunoassay plate, agarose beads, plastic beads, latex beads, immunoblot membranes and immunoblot papers.

19. The invention of Claims 12 or 32, wherein said substrate is latex beads.

10 20. The method of Claim 1, wherein said step of detecting comprises performing assays selected from the group consisting of enzyme-linked immunoassays, radioimmunoassays, immunoprecipitations, fluorescence immunoassays, chemiluminescent assay, immunoblot assays, lateral flow assays, agglutination assays and particulate-based assays.

15 21. The method of Claim 1, wherein said step of detecting comprises:

- (a) contacting said canine  $Fc_\epsilon R$  molecule:IgE complex with an indicator molecule that binds selectively to said  $Fc_\epsilon R$  molecule:IgE complex;
- (b) removing substantially all of said indicator molecule that does not selectively bind to  $Fc_\epsilon R$  molecule:IgE complex; and
- 20 (c) detecting said indicator molecule, wherein presence of said indicator molecule is indicative of the presence of IgE.

22. The method of Claim 21, wherein said indicator molecule comprises a compound selected from the group consisting of a  $Fc_\epsilon R$  molecule, an antigen, an antibody and a lectin.

25 23. The method of Claim 1, said method comprising the steps of:

- (a) immobilizing said canine  $Fc_\epsilon R$  molecule on a substrate;
- (b) contacting said canine  $Fc_\epsilon R$  molecule with said putative IgE-containing composition under conditions suitable for formation of a  $Fc_\epsilon R$  molecule:IgE complex bound to said substrate;
- 30 (c) removing non-bound material from said substrate under conditions that retain  $Fc_\epsilon R$  molecule:IgE complex binding to said substrate; and

(d) detecting the presence of said  $Fc_\epsilon R$  molecule:IgE complex.

24. The method of Claim 23, wherein the presence of said  $Fc_\epsilon R$  molecule:IgE complex is detected by contacting said  $Fc_\epsilon R$  molecule:IgE complex with a compound selected from the group consisting of an antigen and an antibody that binds selectively to  
5 IgE.

25. The method of Claim 24, wherein said compound comprises a detectable marker.

26. The method of Claim 1, said method comprising the steps of:

(a) immobilizing a desired antigen on a substrate;  
10 (b) contacting said antigen with said putative IgE-containing composition under conditions suitable for formation of an antigen:IgE complex bound to said substrate;

(c) removing non-bound material from said substrate under conditions that retain antigen:IgE complex binding to said substrate; and

15 (d) detecting the presence of said antigen:IgE complex by contacting said antigen:IgE complex with said canine  $Fc_\epsilon R$  molecule.

27. The method of Claim 1, said method comprising the steps of:

(a) immobilizing an antibody that binds selectively to IgE on a substrate;

20 (b) contacting said antibody with said putative IgE-containing composition under conditions suitable for formation of an antibody:IgE complex bound to said substrate;

(c) removing non-bound material from said substrate under conditions that retain antibody:IgE complex binding to said substrate; and

25 (d) detecting the presence of said antibody:IgE complex by contacting said antibody:IgE complex with said canine  $Fc_\epsilon R$  molecule.

28. The method of Claim 1, said method comprising the steps of:

(a) immobilizing said putative IgE-containing composition on a substrate;

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(b) contacting said composition with said canine  $Fc_\epsilon R$  molecule under conditions suitable for formation of a  $Fc_\epsilon R$  molecule:IgE complex bound to said substrate;

(c) removing non-bound material from said substrate under  
5 conditions that retain  $Fc_\epsilon R$  molecule:IgE complex binding to said substrate; and

(d) detecting the presence of said  $Fc_\epsilon R$  molecule:IgE complex.

29. The method of Claim 28, wherein said canine  $Fc_\epsilon R$  molecule comprises a detectable marker.

30. The kit of Claim 2, wherein said detection means further comprises an  
10 antigen selected from the group consisting of an allergen and a parasite antigen, wherein said antigen induces IgE antibody production in canids.

31. The kit of Claim 2, wherein said detection means comprises an antibody that selectively binds to canine IgE.

32. The kit of Claim 2, wherein said detection means detects said canine  
15  $Fc_\epsilon R$  molecule.

33. The kit of Claim 30, wherein said antigen is immobilized on a substrate.

34. The kit of Claim 30, wherein said parasite antigen is a heartworm antigen.

35. The kit of Claim 2 further comprising an apparatus comprising:

(a) a support structure defining a flow path;  
20 (b) a labeling reagent comprising a bead conjugated to said antigen, wherein said labeling reagent is impregnated within the support structure in a labeling zone; and

(c) a capture reagent comprising said  $Fc_\epsilon R$  molecule, wherein said capture reagent is located downstream of said labeling reagent within a capture zone  
25 fluidly connected to said labeling zone in such a manner that said labeling reagent can flow from said labeling zone into said capture zone.

36. The kit of Claim 35, wherein said apparatus further comprises a sample receiving zone located along said flow path.

37. The kit of Claim 35, wherein said apparatus further comprises an  
30 absorbent located at the end of said flow path.

38. The kit of Claim 36, wherein said sample receiving zone is located upstream of said labeling reagent.

39. The kit of Claim 35, wherein said bead comprises a latex bead.

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/06774

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 G01N33/566 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 G01N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 97 20859 A (IDEXX LAB INC) 12 June 1997 see claims 6, 7, 10-14, 16-27, 29, 30 see page 1, line 13 - line 21 see page 6, line 15 - line 16 see page 15, line 3 - line 16 see page 29, line 12 - line 25 ---	1-39
X	WO 95 16203 A (GENENTECH INC; TAI WAI FEI DAVID (US); LOWE JOHN (US); JARDIEU PAU) 15 June 1995 see claims 1, 8, 14-16 see page 4, line 18 - page 6, line 9 see page 12, line 25 - page 13, line 5 see page 13, line 14 - line 19 see page 23, line 9 - page 24, line 38 --- -/--	1-39

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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# INTERNATIONAL SEARCH REPORT

Inter. Appl. No.

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## C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 94 29696 A (QUIDEL CORP) 22 December 1994</p> <p>cited in the application</p> <p>see claims</p> <p>see the whole document</p> <p style="text-align: center;">-----</p>	20-39

# INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 98/06774

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